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Human protein C de
Modified GLA domai
Modified GLA domai
                                                                                                                     December 30, 2003, 09:11:15 ; Search time 42 Seconds (without alignments) 166.285 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| SIDSI/gcgdata/geneseq/geneseqp_embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp_embl/AA1980.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                               1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
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AAE8629
AAB82675
AAB82676
AAY18297
AAY18300
AAY18301
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Gapop 10.0 , Gapext 0.5
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Partial human prot
Human protein C Gl
Truncated human pr
Protein C (PC). H
Human protein C de
Human protein C de
Human protein C mu
Modified GLA domai
Modified GLA domai
Human protein C GL
Modified GLA domai
                                                                            Primary structure
Human mature wild
Wild-type human pr
Human protein C de
Human protein C de
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Protein
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AAY18303
AAY18298
AAB36402
AAW75710
AAB56803
AAR35760
AAW72753
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AAU99002
AAU99003
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AAU99006
AAU99007
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AAU99010
AAU99011
AAU99011
       AAB82678
ABB79950
                    AAY18309
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                                                                                                                                                                                                                                                                                                                             Human protein C derivative #1.
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14-MAR-2000; 2000US-0189199
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 WO200159084-A1
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AAE08627;
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Jones BE;

Grinnell BW,

Gerlitz BE,

Human protein C de

ELIL) LILLY & CO ELI.

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N-PSDB; AAD15226
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Matches
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                                                                        Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation, sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy. The present sequence is human protein C derivative
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                                                                                                                                                        Claim 3; Page 46-47; 59pp; English
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14-MAR-2000; 2000US-0189199.
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                WPI; 2001-514662/56.
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                                   N-PSDB; AAD15225
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Matches

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molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial with an anti-platelet agent; protein C described signators. C thrombotic occlusion, thromboelism or stenosis in coronary, cerebral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders
                                                                                                                        Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human protein C derivatives and nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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1 Similarity 79.5%; Pred. No. 1e-21;
35; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                 Claim 4; Page 47-48; 59pp; English
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14-MAR-2000; 2000US-0189199
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2001-514662/56
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Best Local Similarity
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The present sequence is that of a claimed human protein C derivative in which Ser at amino acid position 11 of the mature wild-type protein C sequence (84882673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute
                                                                                                                                                                                                                             "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a
                                                                                                                                                                                                                                                                                262-amino acid heavy chain)"
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arterial thrombotic occlusion, and thromboembolism
"Leu in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                   'note= "gamma-carboxylated"
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14-MAR-2000; 2000US-0189197.
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                               /note=
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59..64
 /note=
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                                                                     Disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                  Domain
molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type forcein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and hemolytic uremic syndrome; sepsis in combination with bacterial thrombotic occlusion, thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboemia grafts in combination with a trombotic occlusion, thromboemia grafts in combination with a trombotytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
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                                                                                                                                                                                                                                             The invention relates to human protein C derivatives and nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gарв
                                                                                                                                     Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.0%; Score 182; DB 22; Length 419; 79.5%; Pred. No. 1e-21; 1ve 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEELRHGSLERECIERICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein C derivative (S11G/Q32E/N33D/L194S).
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                                                   BE;
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                                                                                                                                                                                                           Claim 5; Page 48-49; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82675 standard; Protein; 419 AA
                                                   Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                 Gerlitz BE, Grinnell BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 79.5 tes 35; Conservative
                (ELIL ) LILLY & CO ELI.
                                                                                  WPI; 2001-514662/56.
N-PSDB; AAD15227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 AA;
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Matches
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            C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistantions, but which have increased anticoagulant activity and resistantion to inactivation by serpine compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina).

C vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bacteridal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafte. Human preference of patients with genetically predisposed prothrombotic disorders may
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 The protein is an example of protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercosgulation; sepsis; protein C deficiency; occlusion; thromboembolism; atenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                             Query Match 91.0%; Score 182; DB 22; Length 419; Best Local Similarity 79.5%; Pred. No. 1e-21; Matches 35; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   notes "Asn in wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                              be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Gln in wild-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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 position 194 with Ser.
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                                                                                                                                                                                                                                                                                                                                419 AA;
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                                                                                                                                                                                                                                                                                                                                Sequence
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The present sequence is that of a claimed human protein C derivative in which Ser at position 11 of the mature wild-type protein C in which Ser at position 11 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gly, Gln at position 32 with AB9. Leu at position 32 with Glu, Asn at position 32 with AB9. Leu at position 32 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid candstitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein. A method of producing the derivatives using recombinant creating coronary syndences and disease states predisposing to treating coronary syndences and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina). C vascular occlusive disorders and hypercoagulable states sepsis (in combination with an anti-platelet agent or by local delivery through
                                                                                                                                                                                                                                                                                                                     /note= "activation peptide; removal activates the 2-chain zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
              precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
 "cleavage makes a 2-chain inactive
                                                                                                                                                                                                                                                                                                                                                                     'note= "thrombin cleavage site"
                                                                                                         "gamma-carboxylated"
                                                                                                                                      "gamma-carboxylated"
                                                                                                                                                                    "gamma-carboxylated"
                                                                                                                                                                                                note= "gamma-carboxylated"
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                                                                          "gamma-carboxylated"
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/note= "N-glycosylated"
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14-MAR-2000; 2000US-0189197.
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                                                                                                                                       'note=
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 /note=
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Sequence

8888888

Query Match

Matches

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AAY18297

therapy.

AAY18297
AAY

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This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared ito the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                 GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                            Modified GLA domain of vitamin K-dependent protein.
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Pred. No. 1.9e-21;
0; Mismatches 1
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Best Local Similarity 97.7%;
Matches 43; Conservative
                                                                                                             AAY18300 standard; peptide;
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                    AAY18300;
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                                                                                                 4AY18300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
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                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, ecrebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                      Length 419;
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                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                     ANSFLEELRHGSLERECIEBICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                          1 ANSFLXXLRHGSLXRXCIXXICDFXXAXXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain of vitamin K-dependent protein.
                                                                                                                                                91.0%; Score 182; DB 22; 79.5%; Pred. No. 1e-21; iive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 176; DB 20;
Pred. No. 8.9e-22;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 78; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                             AAY18297 standard; peptide; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.0%;
97.7%;
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                                                                                                                                                                 Local Similarity 79.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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Gaps

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Indels

Modified GLA domain of vitamin K-dependent protein.

1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

Sequence Query Match

Matches

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The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticogulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human cortein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. mycocardial infaction and unstable angina; and disease states predisposing to thrombosis, vascular occlusive disorders and hypercoagulable states e.g. thrombosis, vascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral hamorrhagic fever and permeability increasing protein; thromboic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial cremboility agent, thrombolic disorders in combination with a thrombolic agent, wholeic acid molecules of the invention are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating humans with genetically predisposed prothrombotic disor
by gene therapy. The present sequence is human protein C derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLEELRQGSLERECIEEICDFEEAKEIFEBUDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Best Local Similarity 77.3%; Pred. No. 2.2e-20;
Matches 34; Conservative 0; Mismatches 10
                                                                                                                                                                                                                                                                                                                   Jones BE;
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                                                                 02-FEB-2001; 2001WO-US01221.
                                                                                                                                  11-FEB-2000; 2000US-0181948.
14-MAR-2000; 2000US-0189199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 50-51; 59pp;
                                                                                                                                                                                                                                                                                                               Grinnell BW,
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                                                                                                                                                                                                                                       (ELIL ) LILLY & CO ELI.
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N-PSDB; AAD15228.
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16-AUG-2001
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THE SOUND AND THE STATE OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                        /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                       Location/Qualifiers
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Matches 43; Conservative
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Gaps

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DB 22; Length 419; 10; Indels

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arterial thrombotic occlusion, and thromboembolism
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                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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AAB82678
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                                                                                                                                                                                                                                                                                                                      removal activates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute
                                                                                                                                                                 precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
                                                                                                                                                           "cleavage makes a 2-chain inactive
/note= "His in wild-type protein"
               "Ser in wild-type protein"
                                          note= "Asn in wild-type protein"
                                                          'note= "Leu in wild-type protein'
                                                                                                                                                                                                                                                                                                                                             site"
                                                                                                                                                                                                                                                                                                           | 158..169
| /note= activation peptide;
| 2-chain zymogen
                                                                                                                                                                                                               "gamma-carboxylated"
                                                                                                                                                                                                                                                                          note= "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                           note= "thrombin cleavage
                            note= "Gln in wild-type
                                                                                                                                                                                                                                                                                                                                                           note= "N-glycosylated"
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                                                                         note= "Gla domain"
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14-MAR-2000; 2000US-0189197
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/note= '
               note=
                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BLIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerlitz BE, Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-496919/54.
                                                   Misc-difference 194
                     Misc-difference 32
                                    Misc-difference 33
       Misc-difference 11
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Disulfide-bond
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                                                                                                                     sulfide-
                                                                                        Bulfide
                                                                                               sulfide
                                                                                                                                                                                                                                                                                                               eptide
                                                                  Domain
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The present sequence is that of a claimed human protein C derivative in which His at position 10 of the mature wild-type protein C sequence (see AABS2673) is substituted with Glu, Ser at position 11 with Glu, dlu at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid cubstitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein. While retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardmal infarction and unstable angina), combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitors), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; atemosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein C; human; coronary syndrome; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSFLEELRQGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notes "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Gln in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Asn in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "His in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Thr in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%; Score 174; DB 22; 77.3%; Pred. No. 2.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Leu in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/note= "Gla domain'
Claim 5; Page 54-55; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB82678 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary. Cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variant blood coagulation component, useful for manufacturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medicament for treating or preventing coagulation disorders, e.g. thrombosis, comprises an anticoagulant activity in the protein C-anticoagulant system of blood .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the protein sequence of a mutated Gla
                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein C; Gla domain; human; blood clotting; anticoagulant;
thrombolytic; antiarteriosclerotic; cardiant; antiaggregant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "wild-type Gln substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "wild-type Asn substituted by Asp"
                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLEBLRQGSLERECIEBICDFEBAKBIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "wild-type Asp substituted by
                                                                                                                                                                                                                                                                                                                                         Score 174; DB 22;
Pred. No. 2.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TACT-) TAC THROMBOSIS & COAGULATION AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein C mutated Gla domain SED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page -; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB79950 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                         87.0%;
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                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Misc-difference 23
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                                                                                                                                                                                                                                                                                                     419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB79950;
                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "activation peptide; removal activates the
2-chain zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
                                                                                                                                                                                                   "cleavage makes a 2-chain inactive
precursor (155-amino acid light chain
attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                         "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                     note= "gamma-carboxylated"
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/note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-2000; 2000US-0179801.
14-MAR-2000; 2000US-0189197.
                                                                                                                                          331..345
356..384
156..157
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                                                                 .109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-496919/54.
  Disulfide-bond
Disulfide-bond
Disulfide-bond
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Disulfide-bond
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                                                                                                                                                                                                                                                                              Modified-site
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Peptide

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09-AUG-2001

Claim

Disclosure; Page 79-80; 86pp; English.

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/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
domain (N-terminal amino acids 1-45) of human protein C. The mutated Gla domain contains the substitution mutations D218, Q32E and N33D. Protein C and activated protein C variants comprising a mutated Gla domain are provided by the invention. The variants contain at least 6, and optionally 7-10, amino acid substitutions. A preferred mutant (designated QGNSEDY, see ABB79946) has the mutations H100, S11G, S12N, D23S, Q32E, N33D and H44Y, and shows greatly enhanced anticoagulant activity in standard in vitro coagulation assays. The present mutant (designated SED) was produced in an example from the invention as a step toward the production of the QGNSEDY mutant Gla domain, and shows little,
                                                                                                                                                                                          if any, improvement in anticoggnlant activity over wild-type activated protein C. The invention provides methods for producing the variants based on DNA technology, and with the use of the variants for the treatment of coagulation disorders such as thrombosis or APC resistance, or in diagnostic test systems for assaying components of the protein C-anticoagulant system (all claimed). The variants may also be used in treating arteriosclerosis, myocardial infarction, and disseminated
                                                                                                                                                                                                                                                                                                                                 intravascular coaguiation.
Note: The present sequence is not shown in the specification but is derived from the human wild-type Gla domain sequence given on page 7 of the specification (see ABB79947).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLEELRHSSLERECIEEICSFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 170; DB 23;
Pred. No. 9.1e-21;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY18309 standard; peptide; 44 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Begt Local Similarity 75.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US22152
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                                                                                                                                                                                                                                                                                                                                                                                                                            45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
AAY18309
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                          This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                       Score 168; DB 20; Length 44; Pred. No. 1.9e-20; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                         1 ANSFLXXLRHSSLXRXCIXXICDFXXAFXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  AAY18299 standard; peptide; 44 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 78; 86pp; English.
                                                                                                                                                                                                         84.0%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1999 (first entry)
                                                                                                                                                                                                    Query Match
Best Local Similarity 95.5
Matches 42, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MINU ) UNIV MINNESOTA
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                                                                                                                                                                           44 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9920767-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY18299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy.
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                           Gaps
                                                                                                                                                                                                                                                                                                                                                      1..44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                             ö
 Length 44;
                                                                                                                                                                                                                                                                   GLA domain; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 44;
                           2; Indels
                                                                     ANSFLXXLRESSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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93.2%; Pred. No. 1.9e-20;
live 2; Mismatches 1;
Query Match
Best Local Similarity 95.5%; Pred. No. 1.9e-20;
Matches 42; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14; 86pp; English
                                                                                                                                                  AAY18303 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US22152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0955636
                                                                                                                                                                                                                                       Human protein C GLA domain.
                                                                                                                                                                                                          (first entry)
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Best Local Similarity 93.2
Matches 41; Conservative
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                                                                                                                                                                                                           17-AUG-1999
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                                                                                                                           RESULT 15
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Gaps

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1; Indels

ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH 44

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Search completed: December 30, 2003, 09:18:18 Job time : 43 secs

1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2003
        Copyright
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OM protein - protein search, using sw model

December 30, 2003, 09:16:41; Search time 21 Seconds (without alignments) 201.496 Million cell updates/sec Run on: .

US09497591-1EDITED

200 1 ANSPLXXLRHGSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Regult No.	Score	Query Match	Length	DB	ΙD	Description
-	168	84.0	461	-	KXHU	protein C (activat
7	139	69.5	461	Н	JX0210	υ
m	138	0.69	461	Н	\$18994	protein C (activat
4	121	60.5	456	-	KXBO	υ
2	113	56.5	482	Н	EXRT	coagulation factor
9	109	54.5	492	Н	ЕХВО	
7	108	54.0	488	Н	ЕХНО	
80	100	50.0	443	~	I46932	
Đ	96	49.0	466	٦	KFHU7	
10	84.5	42.2	617	~	S10511	U
11	4	42.2	618	~	A35827	thrombin (EC 3.4.2
12	84	42.0	407	Н	KFBO7	coagulation factor
13	82	41.0	622	-	TBHU	thrombin (EC 3.4.2
14	81	40.5	475	~	ЕХСН	coagulation factor
15	80	40.0	642	~	S53434	plasma protein S p
16	80	40.0	919	Н	KXHUS	plasma protein S p
17	79	39.5	452	ч	A30351	coagulation factor
18	79	39.2	459	~	JQ0419	coagulation factor
19	79	39.5	646	N	S38819	plasma protein S -
20	78	39.0	675	Н	KXBOS	
	94	38.0	675	н	KXRTS	plasma protein S p
22	75	37.5	461	-	KFHU	tion facto
23	73	36.5	642	~	853433	plasma protein S p
24	72	36.0	416	Н	KFBO	tion facto
25	70	35.0	625	Н	TBBO	thrombin (EC 3.4.2
	69	34.5	675	Н	KXMSS	plasma protein S p
27	67.5	33.8	396	-	KXBOZ	
28	63.5	31.8	422	-	KXHUZ	
53	9	30.0	673	~	A48089	

growth potentiatin	growth arrest-spec	probable MAP kinas	probable MAP kinas	probable MAP kinas	hypothetical prote	hypothetical prote	alcohol dehydrogen	primosomal replica	protein-tyrosine k	hypothetical prote	hypothetical prote	ammonium transport	VSG expression sit	protein-tyrosine k	tyrosine kinase re
155476	B48089	D84859	C96575	G96763	T40556	T02367	S27994	G64062	158375	A83512	T25948	E82918	D32433	A48999	JC1189
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674	678	594	603	576	909	1684	558	730	1363	1694	323	510	1235	1298	182
29.5	29.0	28.5	27.3	26.2	26.0	25.0	24.5	24.5	24.5	24.5	24.2	24.2	24.0	24.0	23.5
90	28	56.5	54.5	52.5	25	20	49	49	49	49	48.5	48.5	48	48	47
٥.	7	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

	RESULT 1 KXHU protein C (activated) (EC 3.4.21.69) precursor - human N;Alternate names: autoprothrombin IIA; plasma protein C
	C;Species: Homo sapiens (man) C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999 C;Accession: A22331; A25426; A21781; A23789; A00927 R;Foster, D.C.; Yoshitake, S.; Davie, E.W.
	Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985 A;Title: The nucleotide sequence of the gene for human protein C. A;Reference number: A22331; MUID:85270390; PMID:2991887 A;Accession: A22331
	A; Repidues: 1-461 < POS1>
	A;Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334 R;Plutzky, J.; Hoskins, JA.; Long, G.L.; Crabtree, G.R.
	A:Title: Not. out. out. out. out. out. A.Title: Rolling Evolution and organization of the human protein C gene. A:Reference number: A25426; MUID:86120978; PMID:3511471
	A; Accession: A25426
	A; Wordcust 1.446. 2 Lond A A A A A A A A A A A A A A A A A A A
	A; LIGHE LELELEHICES: GB: M.L. S.W. R. F.
	Proc. Natl. Acad. Sci. U.S.A. Bl, 4766-4770, 1984 A;Title: Characterization of a cDNA coding for human protein C.
	A;Reference number: A21781; MUID:84272714; PMID:6589623 A:Accession: A21781
	A; Molecule type: mRNA
•	R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.; Long, G.L. Nucleic acids Res. 11, 5211-5247, 1985
	Autitle: The structure and evolution of a 461 amino acid human protein C precursor and it
	A; Accession: A23789
	A;Molecule type: mRNA A:Residues: 1-461 cBEC>
	A;Cross.references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
	R;Miletich, J.P.; Broze Jr., G.J. J. Biol. Chem. 265, 11397-11404, 1990
	A,Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation ma a.befarance number, 244605, MITD.00793084, DMTD.1644179
	A; Contention: named a randomydrate binding altes; activation peptide
	A;Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
	J. Biol. Chem. 267, 5102-5107, 1992 J. Biol. Chem. 267, 5102-5107, 1992 J. Biol. Chem. 267, 5102-5107, 1992
	number: A44606; MUID: 92184750; PMID:1544894
	A; Contents: annotation; peta-hydroxyaspartic acid C; Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in:
_	ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also fa

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A/Acce
                                                                                                                                                                                                                                                                   C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction, C;Gene: GDB:PROC A;Gene: GDB:PROC A;Cross-references: GDB:120317; OMIM:176860
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    84.0%; Score 168; DB 1; Length 461;
1 Similarity 72.7%; Pred. No. 4.2e-19;
32; Conservative 2; Mismatches 10; Indels
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein C (activated) (EC 3.4.21.69) precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Lo-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999 C;Accession: S18994; S24312 R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y. submitted to the Rmib Data Library, Pebruary 1992 A;Description: The CDNA clonining and mRNA expression of rat protein C. A;Reference number: S18994
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NyAlternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18389; A18386; A00928
R;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5633-5656; 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                                                  Gaps
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;Title: The cDNA cloning and mRNA expression of rat protein C.;Reference number: S24312; MUID:92329550; PMID:1627650
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     Score 139; DB 1; Length 46
Pred. No. 2e-14;
7; Mismatches 11; Indels
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Best Local Similarity 59.1%; Pred. No. 3e-14;
Matches 26; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                               1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
DB 1;
     Query Match
Best Local Similarity 59.1%;
Matches 26; Conservative
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A; Residues: 1-456 < LON>
R; Fernlund, P.; Stenflo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
Molecule type: mRNA
Residues: 1-461 <OKA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: S18994
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Chem. 257, 12170-12179, 1982

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Pathway: blood coagulation

Suberfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; (Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; (1-23/Domain: signal sequence #status predicted <SIG>
324-40/Domain: propeptide #status predicted <PRO>
525-84/Domain: Gla domain homology <GLA>
741-179/Product: coagulation factor X light chain #status predicted <LCH>
790-121/Domain: EGF homology <EGI>
                                                                                                                                                                                            A; Note: submitted to the EMBL Data Library, June 1994
A; Note: neither the complete nucleic acid sequence nor the complete translation are shown R; Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;232-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #statu F;57-62,90-101,95-110,112-121,129-140,136-149,151-64,172-340,238-243,259-275,388-402,412 F;103/Modified site: erythro-beta-hydroxyaspartic acid (Msp) #status predicted F;187/Binding site: carbohydrate (Ann) (covalent) #status predicted F;208/Binding site: carbohydrate (Ann) (covalent) #status predicted F;218/Binding site: carbohydrate (Ann) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;Molecule type: protein
.;Residues: 183-186, Y. 188-207 <ENJ2>
.;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
hur. J. Haematol. 52, 162-168, 1994
.;Title: Analysis of the partial nucleotide sequences and deduced primary structures of
.;Reference number: I46196; MUID:94222160; PMID:8168596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X79807; NID:gS06600; PIDN:CAAS6202.1; PID:gS06601; Experimental source: Cos-1 cell statistical source: Cos-1 cell source: 109, 890-898, 1991  
Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat statistical statistical statistical source: PS0190; MUID:92041742; PMID:1718949
                                                                                                                                                                                                                                                                                                                                                                                              Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs, Reference number: JC4670; MUID:96194815; PMID:8647460
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183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
183-231/Domain: activation peptide #status predicted <APT>
1232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
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N;Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C:Species: 24.Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
                                                                                              ;Residues: 1-482 <STA1>
;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
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A;Molecule type: DNA
A;Residues: 295-383, G',385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
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A; Accession: S49075
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C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Cuperfamily: coagulation feator X; EGF homology; Gla domain homology; trypein homology C;Eywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F;20-39/Domain: gla domain homology <GLA>
F;30-139/Domain: EGF homology <GLA>
F;30-134/Product: protein C light chain #status experimental <LCH>
F;30-136/Domain: EGF homology <EGS>
F;30-137/Domain: EGF homology <EGS>
F;30-136/Domain: activation peptide #status experimental <APT>
F;30-456/Product: protein C heavy chain #status experimental <F:30-456/Froduct: protein C heavy chain #status experimental <F:30-456/Froduct: protein C heavy chain #status predicted site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F:136/Sid/Binding site: erythro-general (Asp) (covalent) #status predicted F:356/Binding site: erabohydrate (Asn) (covalent) #status predicted
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A;Residues: 197.454, PV" <STE>
B;Resmon, N.L.; DeBault, L.B.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1998
A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless parefracence number: A37541; MUID:83213513; PMID:6304092
A;Reference number: A37541; MUID:83213513; PMID:6304092
A;Contents: annotation; activation; alcium binding
B;Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A;Title: Structural changes required for activation of protein C are induced by Ca2+ bir A;Reference number: A37542; MUID:83213514; PMID:6406503
A;Contents: annotation; activation; calcium binding
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
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A;Reference number: A58498; MUID:96093366; PMID:8578539
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coagulation factor Xa (EC 3.4.21.6) precursor - rat
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-dan-1995 #sequence revision 07-Reb-1997 #text_change 08-Dec-2000
C;Accession: S49075; JC4670; PS0191; PS0190; I62745
R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factor
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                    A;Title: Amino acid sequence of the light chain of bovine protein C. A;Reference number: A18385; MUID:83007325; PMID:6896876 A;Accession: A18385
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J. Balol. Chem. 257, 12180-12190, 1982
A.FITLE: Amino acid sequence of the heavy chain of bovine protein C.
A.FReference number: A18386; MUID:83007326; PMID:6896877
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A,Readdues: 40-194 «FER»
A,Readdues: 40-194 «FER»
A,Note: 82-Lys was aloo found
R,Drakenberg, T.; Pernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A,Title: beta-Hydroxyaspartc acid in vitamin K-dependent protein (A)
A,Reference number: A19316, MUID:83169769; PMID:6572939
A,Contents: annotation; revision to residue 110
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Pred. No. 1.6e-11;
9; Mismatches 12; Indels
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Matches 21; Conservative
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Figure 1971 blood coagulation factor X; EGF homology; Gla domain homology; Clyperfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; Clycewords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam; F;1-15/Domain: signal sequence #status predicted <BIG>
F;1-6-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-180/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EGS>
F;129-164/Domain: EGF homology <EGS>
F;139-392/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-233/Domain: activation peptide #status experimental <AHC>
F;23-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;24-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;24-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;24-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
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F;24-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;24-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;24-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;25-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;26-40-101,95-110,1192-1121,129-140,118-164,172-341/Disulfide bonds: #status experimental <AHC>
F;20/Binding site: sulfate (Tyr) (Covalent) (partial) #status experimental
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Cispecies: Homo sapiens (man)
Cibate: 12-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
Cibate: 12-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
Cisconsion: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A009:
Rileytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5107; 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is the A;Reference number: A24478; MUID:87026600; PMID:3768336
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A/Molecule type: DNA
A/Rocession: A24478
A/Molecule type: DNA
A/Molecule 
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A, Residues: 1-488 <MES>
A, Cross-references: GB MS7285, NID:g182389, PIDN:AAA52421.1; PID:g182390
R; Mido, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
G. Biol. Chem. 267, 7335-7401, 1992
A, Title: Liver-specific expression of the gene coding for human factor X, a blood coagul?
A, Reference number: A42485; MUID:92218390; PMID:1313796
                                                                                                                the proteolytic activation of prothrombin to thrombin in the pre
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A;Title: Isolation and characterization of human blood-coagulation factor X cDNA
A;Reference number: A25853; WUID:86221713; PMID:3011603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 ANSFLEBVKOGNLERECLEBACSLEBAREVFEDAEQTDEFWSKY 84
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Pred. No. 1.5e-09;
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Molecule type: mRNA
A; Residues: 19-284, 'E', 289-488 <KAU>
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Best Local Similarity 43.2
Matches 19; Conservative
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A; Nocie: Deta-lydroxyaspartic acid site

R; Inoue, K.; Morita, T.

R; Inoue, K.; Morita, T.

B; Inoue, K.; Morita, T.

B; Inoue, K.; Morita, T.

A; Note: Deta-lydroxyaspartic acid site

A; Note: Deta-lydroxic bit of O-linked oligosaccharide chains in the activation peptides of A; Reference number: S39414; MUID:94062825; PMID:8243461

A; Note: Deta-lydroxic bit of Sates

A; Note: Carbohydrate binding sites

A; Note: Carbohydrate binding sites

R; Titani, K.; Hermodson, M.A.; Fujkawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D Biochemistry 11, 4899-4903, 1972

A; Titani, K.; Hermodson, M.A.; Ruikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D Biochemistry 11, 4899-4903, 1972

A; Titani, K.; Titani, K.; Davie, E.W.

R; Pujikawa, K.; Titani, K.; Davie, E.W.

R; Pujikawa, K.; Titani, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975

A; Ritle: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to A; Chenter Conversion of A; Note Conversion of Factor Conversion Conve
C; Accession: A22867; A14997; A12030; A34412; S33414; A00925
R; Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A; Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a A; Reference number: A22867; MUID: 84247315; PMID: 6330671
A; Mccession: A22867; MUID: 84247315; PMID: 6330671
A; Mcseldues: 1-487 cFUN>
A; Kessidues: 1-487 cFUN>
A; Kessidues: 1-487 cFUN>
A; Kessidues: 1-487 cFUN>
A; Cross-references: GB: X0673; NID: 9192; PIDN: CAA25286.1; PID: 9193
A; Enfield, D.L.; Ericson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K. Biochemistry 19, 659-667, 1980
A; Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A; Reference number: A14997; MUID: 80130563; PMID: 6766735
A; Mcsession: A14997
A; Molecule type: protein
A; Residues: 41-102, 'N', 104-180 cENF>
B; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
B; McMullen, B.A.; Fujikawa, K.; Enfield, D.L.; Ericson, L.H.; Walsh, K.A.; Neurath, H.
B; Contents: annotation; revision to residue 103
A; Reference number: A20274; MUID: 83308813; PMID: 668856
A; Contents: annotation; revision to residue 103
B; Title: The Acad. Sci. U.S.A. 72, 3082-3086, 1978
A; Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A; Reference number: A12030; MUID: 76053069; PMID: 1059093
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R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of tw
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A;Gene: F10
A;Map position: 13q34
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M.Rebidues: 183-292,294-295, 'GDE', 299-334,336-348,'AE',351-354,356-441,'GKFG',446-492 <1
A,Rebidues: 183-292,294-295, 'GDE', 299-334,336-348,'AE',351-354,356-441,'GKFG',446-492 <1
A,Rebidues: carbohydrate binding sites and disulfide bonds were determined
R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
Baol. Chem. 264, 16897-16904, 1989
A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A;Reference number: A34412; MUID:89380326; PMID:2789221
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A, Accession: A34412 A, Molecule type: protein A, Residues: 85-126 <PER>

activation.

A; Accession: A12030

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Gaps ; 0

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Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #text_change 08-Dec-2000
C;Accession: A28322, A23819; A31186; B31186; S63524
R;O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murrie Proc. (Natl. Acad. Sci. US.A. 84; S158-S162, 1987
A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende A;Reference number: A28322; MUID:87260948; PMID:3037537
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Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.; iochemistry 27, 7785-7793, 1988
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental F;221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental F;234,235/Clbarding site: carbohydrate (Asn) (covalent) #status experimental F;234-235/Clbarding site: Arg-11e (coagulation factor 1Xa, coagulation factor VIIa) #statu F;276,322,419/Active site: His, Asp, Ser #status experimental
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A;Reference number: A90539; MUID:89088153; PMID:3264725
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C;Species: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C;Accession: 146932
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 234-238, 1993
A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A;Reference number: 146932; MUID:93190306; PMID:8383365
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-443 cBRO>
A;Cross-references: GB:S56300; NID:9266294; PID:9266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;24-83/Domain: Gla domain homology cGLA>
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A;Molecule type: DNA
A;Residues: 1-466 -COHA>
A;Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
A;Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart,
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A;Title: Characterization of a cDNA coding for human factor VII.
A;Reference number: A23819; MUID:8620595; PMID:3486420
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3.9e-08;
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Pred. No. 2.2e-09;
8; Mismatches 17
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ive 5; Mismatches
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Best Local Similarity 43.2%;
Matches 19; Conservative E
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nes 19; Conservative
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Matches 19
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A; Residues: 1-23 - RES>
A; Crose-references: GB: M32397; NID:g183860; PIDN:AAA52636.1; PID:g553330
B; Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla
A; Title: Structure of human dest[1-45] factor Xa at 2.2 angstroms resolution.
A; Reference number: A49458; MUID:93360277; PMID:8355279
A; Contents: annotation; X-ray crystallography, 2.2 angstroms
C; Comment: The two chains held together by one disulfide bond are formed from a single-c
C; Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig9-164/Domain: EdF homology <EG2>
Fi183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
Fi183-488/Product: coagulation factor X heavy chain #status experimental <APT>
Fi183-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
Fi183-462/Domain: trypsin homology <TRY>
Fi233-462/Domain: trypsin homology <TRY>
Fi46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
Fi57-62/Disulfide bonds: #status predicted
Fi90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA; Residues: 13.284, E', 289-488 <LB2>; Residues: 13.284, E', 289-488 <LB2>; Residues: 13.284, E', 289-488 <LB2>; Cross-references: CB:KO1886
; McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, B.Y.; Weins iochemistry 22, 2875-2884, 1983
; Chemistry 22, 2875-2884, 1983
; Title: Complete amino acid sequence of the light chain of human blood coagulation fact; Reference number: A20362; MUID:83257207; PMID:6871167
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                                                                                                                                                                     coding for human blood coagulati
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A; Residues: 183-234 < 1NO>
A; Note: 1917cosylation sites
A; Note: identification and characterization of beta-hydroxyaspartic acid
B; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G.
Game 84, 517-519, 1989
A; Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A; Reference number: 154051; MUID:90128299; PMID:2612918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modecule type: protein
,Modecule type: protein
,Residues: 41-179 «MCM»
,Inoue, K.; Morita, T.
ur. J. Biochem. 218, 153-163, 1993
,Title: Identification of O-linked oligosaccharide chains in the activation peptides
,Reference number: S39414; MUID:94062825; PMID:8243461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
;Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336; Pung, M.R.; Hay, C.W.; MacGillivray, R.T.A. roc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985 roc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985 roc. Sci. Characterization of an almost full-length cDNA coding for human; Reference number: A22208; MUID:85216545; PMID:2582420
                                                                                                                                                                                                                                                                                                                               ;Molecule type: mRNA, Readudes: 13-41, SV, 443-488 <FUN>, Readudes: 13-41, SV, 443-488 <FUN>, Readudes: 13-441, SV, 443-488 <FUN>, SCOBSTEFERENCES: GB:KO3194; NID:G182840; FIDN:AAA52490.1; FID:g182841; Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W. xoc. Natl. Acad. Scl. U.S.A. 81, 3699-3702, 1884, Title: Characterization of a cDNA coding for human factor X. Reference number: A21284; MUID:84222026; PMID:6587384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: translation not shown; translated from GB/EMBL/DDBJ
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A;Map posttion: 13q34-13q34
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Pathway: blood coagulation C.Superfamily: coagulation fact C.Keywords: beta-hydroxyaspart: F:1-23/Domain: signal sequence F:24-40/Domain: propeptide Hent: F:55-84/Domain: Gla domain home: F:41-179/Product: coagulation i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A20362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S39415
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42.2%; Score 84.5; DB 2; Length 618;
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A, Reterence mumorer: 803524; FULLD: 902020; FULL: 902020; A, Accession: 863524
A, Residues: 61-65; 99-103; 105-109; 213-217; 308-312 < PER>
C, Genetics:
C, Genetics:
A, Genetics:
A, Genetics:
C, Superior: 1334-13434
A; Introms: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
A; Introms: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C, Function:
A, Pathway: blood coagulation extrinsic pathway
C, Superfamily: organization factor X; EGF homology; Gla domain homology; trypsin homology
C, Keywords: beta-hydroxyaspartic acid; blood coagulation: calcium binding; carboxyglutam
F,1-20/Domain: signal sequence # Heatus predicted < SIG>
F,45-104/Domain: Gla domain homology < GLA>
F,45-104/Domain: Gla domain homology < GLA>
F,10-1141/Domain: EGF homology < EGA>
F,110-114/Domain: EGF homology < EGA>
F,111-114/Domain: EGF homology < EGA>
F,111-114/Tomain: EGF homology < EGA-
F,111-1
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S10511
thrombin (EC 3.4.21.5) precursor - rat
thrombin (EC 3.4.21.5) precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C.Accession: $10511, A60576; B42696
R.Dibhanich, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A.Title: cDNA sequence of rat prochrombin.
A.Accession: $10511
A.Molecule type: mRNA
A.Accession: $10511
A.Acce
A;Residues: 61-212 <THI>
A;Recession: B31186
A;Accession: B31186
A;Molecule type: protein
A;Residues: 213-466 <TH2>
R;Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A;Contents: annotation; carbohydrate binding sites
A;Contents: annotation; carbohydrate binding sites
B;Persson, B.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A;Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A;Reference number: S63524; MUID:96096752; PMID:8529655
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Rybote: the authors purified the proenzyme from the estrogen-stimulated maturing rat uter RyBanfield, D.K.; MacGillivray, R.T.A.
RyBanfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-7783, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-7783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seqn. A;Reference number: A42696, MUID:92212913; PMID:1557383
A;Accession: B42696
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 383-617, E' ABAN>
A;Residues: 383-617, E' ABAN>
A;Cross-references: GB:M81397
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Reywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydropit-124/Domain: signal sequence #status predicted ASIG>
F;28-88/Domain: Gla domain homology AGLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;44-617/Product: prothrombin #status experimental <PMAT>
F;109-187/Domain: kringle homology <KR1>
F;109-187/Domain: kringle homology <KR2>
F;215-292/Domain: kringle homology <KR2>
F;500-51.58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;50,51.58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5f
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A;Molecule type: mRNA
A;Residues: 1-618 cDEG
A;Residues: 1-618 cDEG
A;Residues: 1-618 cDEG
A;Cross-references: GB:X52308; NID:g53813; PIDN:CAA36548.1; PID:g53814
A;Experimental source: strain C57BL/6
A;Note: the data ware obtained from females resulting from the cross of M. domesticus and R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Tilla: Partial characterization of vertebrate prothrombin cDNAs: amplification and seqn. A;Reference number: A42696; MUID:92212913; PMID:1557383
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A;Residues: 384-618,'E' < BAN>
A;Rolecule type: mRNA
A;Residues: 384-618,'E' < BAN>
A;Rolecule type: mRNA
A;Residues: 384-618,'E' < BAN>
A;Residues: 384-618,'E' < BAN-
A;Residues: 384-618,'E' < BAN-
A;Residues: 384-618,'E' < BAN-
A;Residues: 384-618,'E' < BAN-
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Reywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydrc
F;25-43,Domain: sprothrombin B #stratus predicted < MAT>
F;28-88,Domain: kringle homology < GLA>
F;34-618,Product: prothrombin B #stratus predicted < MAT>
F;315-293,Domain: kringle homology < RR2>
F;361-610,Domain: kringle homology < RR2>
F;361-610,Domain: kringle homology < RR2>
F;50.51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;50.51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,56
F;403,459,565/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANS-FLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPODTDVFWAKY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.2%; Score 84.5; DB 2; Length 6
Best Local Similarity 42.2%; Pred. No. 1.8e-05;
Matches 19; Conservative 5; Mismatches 20; Indels
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A; Molecule type: protein
A; Readdues: 315-334, Nv, 336-348, Nv, 350-368, Nv, 370-397, Nv, 399-413, Nv, 415-484, Nv, 486-4
R; Readdues: 315-334, Nv, 336-348, Nv, 350-368, Nv, 370-397, Nv, 399-413, Nv, 415-484, Nv, 486-4
R; Readdues: 315-334, Nv, 136-31215, 1986
A; Reference number: A37551; MUID: 87008532; PMID: 3759958
A; Contents: annotation; activation cleavages
R; Macdillivray, Rr.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.
A; Ann. N. Y. Acad. Sci. 485, 73-79, 1986
A; Title: Recombinant genetic approaches to functional mapping of thrombin.
A; Reference number: IS1952; MUID: 87182874; PMID: 3471151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-2, RI'.5-100 cRES.
A; Residues: 1-2, RI'.5-100 cRES.
A; Cross-references: GB:M3031; NID:9190723; PIDN:AAA60220.1; PID:9190724
A; Cross-references: GB:M3031; NID:9190723; PIDN:AAA60220.1; PID:9190724
C; Comment: Troombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C; Comment: Prochrombin is activated on the surface of a phospholipid membrane that binds
ter 314-Arg, are released in natural blood clotting.
C; Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxyl
C; Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxyl
c; Comment: The prothrombin precursor is synthesized in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:119894; OMIM:176930
A;Map position: 11p11-11q12
A;Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552,
A;Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552,
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: acute phase; blood coaquiation; calcium binding; carboxyglutamic acid; duplic
F;1-24/Domain: signal sequence #status predicted <SIG>
F;28-43/Domain: gropeptide #status predicted <PRO>
F;28-43/Domain: Gla domain homology <GLA>
F;44-622/Product: prothrombin #status experimental <APT>
F;44-527/Domain: activation peptide #status experimental <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 44-118,'N',120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-308,'
Bibtkowski, R.J.; Blion, J.; Downing, M.R.; Mann, K.G.
J. Biol. Chem. 252, 4942-4957, 1977
A;Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A;Reference number: A37550; MUID:77207112; PMID:873923
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F;49,50,57,59,62,63,68,68,67,27,75,Modified site: gamma-carboxyglutamic acid (Glu) #status
F;60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
F;121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Characterization of the complementary deoxyribonucleic acid and gene coding; Reference number: A00914; MUID:83231469; PMID:6305407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A00914
A;Molccule type: mm.
A;Residues: 8-163, N',165-622 <DE2>
A;Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344
                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:M17262, GB:M33691, NID:9558069, PIDN:AAC63054.1, PID:9339641; Degen, S.J.F., MacGillivray, R.T.A.; Davie, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;108-186/Domain: kringle homology «KR1»
;213-291/Domain: kringle homology «KR2»
;238-361/Product: thrombin light chain #status experimental «LCH»
;364-622/Product: thrombin heavy chain #status experimental «HCH»
                                                  Biochemistry 26, 6165-6177, 1987
A;Title: Nucleotide sequence of the gene for human prothrombin.
A;Reference number: A29351; MUID:88077877; PMID:2825773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: B00914
A, Molcaule type: DNA
A, Residues: 188-311 - DE3>
R; Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A, Reference number: A37549; MUID: 77193964; PMID: 266717
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A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-622 <DEG>
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                                                                                                                                                                                               Accession: A29351
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A Regidues: 58-62, X', 64-68 eMCM>
A; Regidues: 58-62, X', 64-68 eMCM>
A; Note: the residue designated 'X' was determined to be hydroxyaspartic acid
B; Hase, S: Kawabata, S: Nishimura, H:; Takeya, H:; Sueyoshi, T:; Miyata, T:; Iwanaga,
J: Blochmen: 104, 867-868, 1988
A; Tille: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A; Contenn: annotation
A; Note: structure and location of covalently bound carbohydrate
C; Function:
A; Description: catalyzes the proteolytic activation of coagulation factor X in the prese
gulation factor IX in the presence of calcium and tissue factor
A; Description: catalyzes the proteolytic activation of coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-152/Froduct: coagulation factor VII a light chain #status experimental eMal>
F; 1-44/Domain: EGF homology eEG2>
F; 1-127/Domain: EGF homology eEG3>
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A;Molecule type: protein
A;Molecule type: protein
A;Molleu; B.A.; Fujikawa, K.; Kisiel, W.
B;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Accession: C20274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coagulation factor VIIa (EC 3.4.21.21) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1990 Heaquece_revision 23-Mar-1995 #text_change 16-Jul-1999
C;Accession: A31979; C20214
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, J. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII: Its purification and complete amino acid sequence. A;Reference number: A31979; MUID:89008362; PMID:3049594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombin (EC 3.4.21.5) precursor [validated] - human N;Alternate names: coagulation factor II N;Contains: prothrombin (C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000 C;Accession: A29351; A00914; B00914; A37549; A37550; I51952
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.4e-05;
3; Mismatches 20; Indels
                                                                                                                                                                                                                    44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88
                                                                                                                                                  1 ANS-FLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Pred. No. 1.8e-05;
5; Mismatches 20; Indels
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                                                  5; Mismatches
42.28;
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Best Local Similarity 43.9%;
Matches 18; Conservative
                                             19; Conservative
Best Local Similarity
Matches 19; Conserv
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RESULT 13

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C;Accession: S53434
R;Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A;File: Identification of candidate residues for interaction of protein S with C4b binds A;Reference number: S53433; MUID:95134217; PMID:7832752
A;Recession: S53434
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat homore; 1-51/Domain: Gla domain homology (fragment) <GLA>
F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F;8-642/Froduct: plasma protein S #status predicted <MAT>
F;87-120/Domain: EGF homology <EG1>
    plasma protein S precursor, vitamin K dependent - rhesus macaque (tragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;127-165/Domain: EGF homology <EG2>
F;171-207/Domain: EGF homology <EG3>
F;211-248/Domain: EGF homology <EG3>
F;211-633/Domain: BGF homology <EG3>
F;211-633/Domain: BGF homology <EG8>
F;211-633/Domain: Jaminin G repeat homology <CG8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 36.4%; Pred. No. 9.8e-(
Matches 16; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: tissue type liver A, Note: the source is designated as rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:L31380
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-642 < GRE>
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C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Keywords: beta-hydroxyasparic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-40/Domain: grapeptide #status predicted <PRO>
F; 25-84/Domain: Gla domain homology <GLA>
F; 41-185/Product: coagulation factor X light chain #status experimental <LCH>
F; 90-121/Domain: EGF homology <EGJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N;Alternate names: virus-activating proteinase
C;Species Gallus Gallus (chicken)
C;Decies Gallus Gallus (chicken)
C;Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: S15838; S20380; $20381
K;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na FEBS Lett. 283, 281-285, 1991
A;Title: Primary structure of the virus activating protease from chick embryo. Its ident
A;Reference number: S15838; MUID:91257322; PMID:2044767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;241-468/Domain: trypsin homology <TRY>
F;241-468/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #8
F;46,47,54,56,59,60,65,66,69,72,75,73,72,748,77-2348,747-252,757-283,396-410,42
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;282,328,425/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-475 <SUZ>
A; Residues: 1-475 <SUZ>
A; Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870
R; Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1995
A; Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A; Reference number: S20380; MUID:92164779; PMID:1537403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:129-167/Domain: EGF homology <EG2>
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
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                                        F;391-407/Disulfide bonds: #status experimental
F;406,462/Active site: His, Asp #status predicted
F;416/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;568/Active site: Ser #status experimental
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8 ANSMLETTKOGNLERECIEELCNKEEAREVFENDPETDYFYPKY 51
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MEDLINE=92305321; PubMed=1611081;
Sugahara Y., Miura O., Yuen P., Aoki N.;
"Protein C deficiency Hong Kong 1 and 2: hereditary protein C deficiency caused by two mutant alleles, a 5-nucleotide deletion and a missense mutation.";
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MEDLINE=97157472; PubMed=9003757;
Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,
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MEDLINE=91329836; PubMed=1868249;
Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
"The spectrum of genetic defects in a panel of 40 Dutch families wi
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Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
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                                                                                                                                                                                                           the human antithrombotic
                                     Harris R.J., Ling V.T., Spellman M.W.; "O-linked fucese is present in the first epidermal growth factor domain of factor XII but not protein C."; J. Biol. Chem. 267:5102-5107(1992).
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"Protein C deficiency: a database of mutations. For the Protein Subcommittee of the Scientific and Standardization Committee of International Society on Thrombosis and Haemostasis.";
Thromb. Haemost. 69:77-84 [1993].
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Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
Sala N., Cooper D.N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87204221; PubMed-2437584;
Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Protein CVermont: Symptomatic type II protein C deficiency associated with two GLA domain mutations.";
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Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer
Rainville I.R., Long G.L.;
                                                                                                                                                                                     Fisher C.L., Greengard J.S., Griffin J.H.;
"Models of the serine protease domain of the human ar
plasma factor activated protein C and its zymogen.";
Protein Sci. 3:588-599(1994).
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MEDLINE=90098906; PubMed=2602169;
                 MEDLINE=92184750; PubMed=1544894;
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MEDLINE=92380660; PubMed=1511988;
                                                                                                                                             3D-STRUCTURE MODELING OF 175-450.
MEDLINE=94272342; PubMed=8003977;
                                                                                                                                                                                                                                                                                                                                                                               "The 2.8 A crystal structu
EMBO J. 15:6822-6831(1996)
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VARIANTS GLY-14; GLN-211; TYR-244; GLN-253; LEU-321; CYS-328; ILE-385 Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C., Koerper M.A., Coughlin J., Griffin J.H.; "Genetic mutations in ten unrelated American patients with symptomatic type 1 protein C deficiency."; Blood Coagul. Fibrinolysis 4:791-796(1991). . Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E., Wada H., Deguchi K., Shirakawa S., Saito H.; Homozygous protein C deficiency: identification of a novel missense mutation that causes impaired secretion of the mutant protein C."; J. Lab. Clin. Med. 119:682-689(1992). Cooper D.N.; protein C (PROC) the protein C anticoagulant Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E., Juhan-Vaguu I., Alach M.; Five novel mutations located in exons III and IX of the protein C gene in patients presenting with defective protein C anticoagulant "A Gla domain mutation (Arg 15-->Trp) in the protein C (PROC) gene causing type 2 protein C deficiency and recurrent venous MEDLINE-94(01666; PubMed-8398832; Marchetti G., Patracchini P., Gemmati D., Castaman G., Rodeghiero i Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.; "Symptomatic type II protein C deficiency caused by a missense mutation (Gly 381-->Ser) in the substrate-binding pocket."; Br. J. Haematol. 84:285-289(1993). Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.; "A novel homozygous missense mutation in the protein C (PROC) gene causing recurrent venous thrombosis."; "Twelve novel and two recurrent mutations in 14 Austrian families with hereditary protein C deficiency."; Blood Coagul. Pibrinolysis 4:273-280(1993). VARIANTS ARG-145; LEU-210; TRP-211; THR-243; LEU-321; MET-340 AND Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M., Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.; "Two novel mutations responsible for hereditary type I protein C deficiency: characterization by denaturing gradient gel THR-388 AND VAL-388. MEDLINE=33271391; PubMed=8499565; Poort S.R.; Pabinger-Fasching I., Mannhalter C., Reitsma P.H., Bertina R.M.; Millar D.S., Grundy C.B., Bignell P., Moffat B.H., Martin R., Kakkar V.V., Cooper D.N.; VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294 MEDLINE=93313192; PubMed=8324221; Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., "Two different missense mutations at Arg 178 of the gene causing recurrent venous thrombosis."; Hum. Genet. 89:685-686 (1992). thrombosis."; Blood Coagul. Fibrinolysis 4:345-347(1993) MEDLINE=93250852; PubMed=1301959; MEDLINE=92380661; PubMed=1511989; VARIANT SER-334. MEDLINE=92276939; PubMed=1593215; MEDLINE=93271396; PubMed=8499568; MEDLINE-94122329; PubMed-8292730; VARIANTS GLN-220 AND TRP-220 Hum. Mutat. 1:491-500(1992). Genet. 89:683-684 (1992) activity."; 31ood 82:159-168(1993). electrophoresis." VARIANT GLN-220 VARIANT SER-423 VARIANT TRP-57 [20]

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-1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE BUZYME IS THEN ACTIVATED BY THROMEIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS STRONGLY PROMOTED BY THROMBOMOULIN.

-1- TISSUE SPECIFICITY: PLASNA; SYNTHESIZED IN THE LIVER.
-1- PTM: THE VITAMIN K-DEPENDENT, BIXTHESIZED IN THE LIVER.
-1- PTM: THE VITAMIN K-DEPENDENT, BIXTHESIZED IN THE LIVER.
-1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER, SITE, BEYOND THE GLAD DOWAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCENTION OF THE THROMBOMOULIN COMPLEX.
-1- SIMILARITY: BELONGS TO PEPTINASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A comparative study or parties," region of mammalian protein C.";
region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994)
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEINS THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
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Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                       PRTC_MOUSE STANDARD; PRT; 461 AA.
P313587; 035498;
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprochrombin IIA) (Anticoagulant protein C) (Blood coagulation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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            Length 461;
                                    10; Indels
                                                                44
                                                                             1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
        Score 160; DB 1;
Pred. No. 6.1e-21;
2; Mismatches 10;
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BROSITE; PSCOLLO; TRYESIN_BROSIN; Hydroxylation; KW Gamma-carboxyglutemic acid; Calcium-binding; Vitemin K; Hydroxylation; KW Gamma-carboxyglutemic acid; Calcium-binding; Vitemin K; Hydroxylation; KW Gamma-carboxyglutemin Calcium-binding; Vitemin K; Hydroxylation; FT SIGNAL

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199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).

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(BY SIMILARITY).

(BY SIMILARITY).

GAMMA-CARBOXYGLUTAMIC ACID

(BY SIMILARITY).
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(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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ITE; PS00010; ASX_HYDROXYL; 1.

ITE; PS01022; BGF 1; 1.

ITE; PS01186; BGF 2; 2.

ITE; PS01187; BGF CA; 1.

ITE; PS00011; GLU_CARBOXYLATION; 1.

ITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006209; EGF_Iike.
InterPro; IPR001283; GLA_blood.
InterPro; IPR001284; SCI_Drotease_Try.
InterPro; IPR001294; VitK_dep_GLA_
Pfam; PF00008; EGF; 2.
Pfam; PF000089; EGF; 2.
Pfam; PF000089; Lrypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR0001; GLABLOOD.
SWART; SM00069; GLA; 1.
SWART; SM00069; GLA; 1.
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InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                               EGF Ca.
EGF_like.
GLA_blood.
                                                                                                                   EMBL; D10445; BAA01235.1; -. EMBL; AF034569; AAC33795.1; - EMBL; D43755; BAA07812.1; -. PIR; JX0210; JX0210 HSSP; P04070; 1PCU.
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MEROPS; S01.218; -.
MGD; MGI:97771; Proc.
                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001881;
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INTERPRO; PRR00135; ARX_hydroxyl.
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INTERPRO; IPR001314; Chymotrypsin.
INTERPRO; IPR001381; EGF_Ca.
INTERPRO; IPR002393; GLA_blood.
INTERPRO; IPR001254; Ser_Drotease_Try.
INTERPRO; IPR001254; Ser_Drotease_Try.
INTERPRO; IPR001254; Ser_Drotease_Try.
INTERPRO; IPR001254; Ser_Drotease_Try.
INTERPRO; IPR001254; GLA_blood.
PRINTS; PR00122; CHYMOTRYPSIN.
PRINTS; PR001202; CHYMOTRYPSIN.
PRNSTT; SM00129; EGF_CA; 1.
SWART; SM00129; EGF_CA; 1.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS011186; EGF_2; 2.
PROSITE; PS011186; EGF_2; 2.
PROSITE; PS010134; TRYPEIN DOM; 1.
PROSITE; PS010134; TRYPEIN DOM; 1.
     or send an email to license@isb-sib.ch)
                                       EMBL; X64336; CAA45617.1;
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                                                          PIR; S18994; S18994.
HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
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       -!- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMEIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS STRONGLY PROMOTODED BY THROMENON OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTODED BY THROMENONIN.
-!- TISSUE SPECIFICITY: PLASNA; SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-!- MISCELLANGOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCENTION OF THE THROMENONULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS.PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE-92329550; PubMed-1627650;

MEDLINE-92329550; PubMed-1627650;

MEDLINE-92329550; PubMed-1627650;

MEDLINE-92329550; PubMed-1627650;

"The CDNA cloning and mRNA expression of rat protein C.";

Biochim. Biophys. Acta 1131:329-332(1992).

-!- FROUTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattue norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
factor XIV).
                                                                                                                                               . .) (POTENTIAL).
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Pred. No. 5.8e-16;
7; Mismatches 11; Indels
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01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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PROSITE; PRO134; TRYPSIN_nr., PROSITE; PRO134; TRYPSIN_SER; I.
PROSITE; PS00135; TRYPSIN_SER; I.
Blood coagulation; Glycoprotein; Serine protease;
Blood coagulation; Glycoprotein; Serine protease;
Blood coagulation; Glycoprotein; Serine protease; Signal.
SGNAL BY SIMILARITY.
PROPEP 33 41 BY SIMILARITY.
PROPEP 34 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
CHAIN 199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
CHAIN 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).
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   SO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY AND THE PROPERTY OF THE PROPER
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-!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUE SEBIOUES ALLOWS THE MODIFIED PROTHEN TO BLIND CALCIUM.
-!- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCENITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PERTIDASE FAMILY SI.
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb-sib.ch).
                                                                                                                                                                                                                                                         RESULT 4
PRTC RABIT

ID PRTC RABIT

AC 028661,

AC 028661,

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Vitamin F-Gependent protein C precursor (EC 3.4.21.69)

DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation precior XIV) (Fragment).

Factor XIV) (Fragment).

"hordata; Craniata; Vertebrata; Euteleostomi;

"hordata; Craniata; Creniata; Creniagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen L., He X., Dahlback B.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REQULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                        Gaps
                 BY SIMILARITY. (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                    69.0%; Score 138; DB 1; Length 461; 59.1%; Pred. No. 8.7e-16;
                                                                                                                                                    11; Indels
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                                                                                   8A4CF93664EDACD5 CRC64;
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SIMILARITY
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF Like.
InterPro; IPR002383; GLA_blood.
387
426
215
N-
291
355
N-
51912 MW;
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                                                                                                                                                        Conservative
 373
398
215
291
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461 AA,
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26; Conserv
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TISSUE=Liver;
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DISULPID
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BY SIMILARITY.

BY SIMILARITY.

VITAMIN K-DEPENDENT PROTEIN C.

PROTEIN C LIGHT CHAIN (BY SIMILARITY).

PROTEIN C HEAVY CHAIN (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).

CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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InterPro; IPR001254; Ser protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00009; EGF; 2.
Pfam; PF00099; Ia; 1.
Pfam; PF00099; ixypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
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DR Pfam; PF00008; EGF; L.

DR Pfam; PF00089; LTYPSin; 1.

DR PFam; PF00089; LTYPSin; 1.

DR PRINTS; PR00722; CHYMOTRYEIN.

DR PRINTS; PR00012; CHYMOTRYEIN.

DR SWART; SM0004; GLA; 1.

DR SWART; SM00004; TATP SPC; 1.

DR PROSITE; PS00025; EGF 1; 1.

DR PROSITE; PS001167; EGF 2; 2.

DR PROSITE; PS001167; EGF 2; 2.

DR PROSITE; PS001167; EGF 2; 1.

DR PROSITE; EGF 2; 
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51866 MW;
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52.3%;
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459 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBDATT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
--- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
--- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
--- MISCELLANBOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains."; Life Sci. 58:148-159 (2001).

-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21121490; PubMed=11229814;
Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
Kim H.K.W.;
                                                       Gaps
                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
24-FEB-2003 (Rel. 41, Last annotation update)
(Automin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                       .<u>`</u>
                                  Pred. No. 1.3e-15;
4; Mismatches 14; Indels
                                                                                        44
                                                                                                           37 ANSFLEELRPSSLERECVEEVCDLEEAKEIFQSVDDTLAFWYKY 80
                                                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY; Contains 2 EGF-like domains.
                                                                                                                                                                                                             459 AA.
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InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
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EGF like.
GLA blood.
IEGF.
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                                  59.1%;
                                                    26; Conservative
                                                                                                                                                                                                             STANDARD;
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                                   Best Local Similarity
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID (BY
SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                   GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                                           GAMMA-CARBOXYGLUTAMIC ACID
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Pred. No. 4.8e-13;
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STRONGLY PROMOTED BY THROMBOMODULIN
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PEPTIDE
DOMAIN
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SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPERTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROCESSING, AND CALCIUM-BINDING DATA.

MEDLINE=83213514; PubMed=6406503;
Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;

Structural changes required for activation of protein C are induced by Ga2+ binding to a high affinity site that does not contain gamma-carboxyglutamic acid.";

-I FUNCTION: PROTEIN C IS A. VITAMIN K.DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VAND VILIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-I CANALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIINE=85014875; PubMed=6091100;
Long G.L., Balagaje R.M., McGillivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bovine protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83213513; PubMed-6304092;
Esmon N.L., Debault L.E., Esmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-
                                                                                                                                     13-JUL-1986 (Rel. 01, Created)
13-JUG-1987 (Rel. 05, Last sequence update)
13-SEP-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-83169769; PubMed=6572939;
Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
"Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=83007326; PubMed=6896877; Stentlo J., Fernlund P., Stentlond C., Stentlond C., Stentlond C., Stentlond acid sequence of the heavy chain of bovine protein C."; J. Biol. Chem. 257:12180-12190(1982).
                                                                                                                                                                                                                                                                                                                                                                                                           Fernlund P., Stenflo J.; "Amino acid sequence of the light chain of bovine protein C."; J. Biol. Chem. 257:12170-12179(1982).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.
MEDLINE=833007325; PubMed=6896876;
  14; Indels
                                      |||||| || || || || || ANSFLEELRPSSLERECKEETCDFEEAREIFONTENTMAFWSKY 85
                         ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                                                                                                456 AA
 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 258:5548-5553(1983).
23; Conservative
                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domainless protein C.
                                                                                                                                                                                                                              taurus (Bovine)
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PRTC_BOVIN
P00745;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIGNAL <1 29
PROPEP 30
-!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPRNDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIPIED PROTEIN TO BIND CALCIUM.
-!- MISCELLANBOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCGNITION OF THE THROMEIN-THROMBONDULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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PROTEIN C HEAVY CHAIN.
ACTIVATION PEPTIDE.
EGF-LIKE 1.
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CHARGE RELAY SYSTEM
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SERINE PROTEASE.
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PROSITE; PSOIL86; EGF_2; 2.
PROSITE; PSOIL87; EGF_CA; 1.
PROSITE; PSOOOIL; GLU CARBOXYLATION; 1.
PROSITE; PSOO134; TRYPSIN DOM; 1.
PROSITE; PSOO135; TRYPSIN HIS; FALSE_NEG.
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InterPro; IPR00289; EGF_Tike.
InterPro; IPR002393; GLA_blood.
InterPro; IPR002210; IEGF_.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; VitK_dep_GLA.
Fam; PP00008; EGF; 2.
Pfam; PP00594; 9la; 1.
Pfam; PR00722; CHYWOTRYPSIN.
PRINTS; PR00702; CHYWOTRYPSIN.
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SMART; SM00069; GLA; 1.
SMART; SM00020; TYP2 SPC; 1.
PROSITE; PS00010; AST HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
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Chymotrypsin
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InterPro; IPR001314;
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Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975)
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J. Biol. Chem. 267:19642-19649(1992).
                                                                                                                                     with mammalian serine proteases.";
Biochemistry 11:4899-4903(1972).
                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 261:4008-4014(1986)
                                                                                                                                                                                                                                                                                                   MEDLINE=86140210; PubMed=3949800;
                                                                                                  MEDLINE=73053314; PubMed=4264286;
                                                                                                                                                                        MEDLINE=76053121; PubMed=1059122;
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                                                                                                                     Neurath H., Davie E.W.;
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MEDLINE-76053069; PubMed=1059093;
Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-487 FROM N.A.
MEDLINE=84247315; PubMed=6330671;
Fung M.R., Campbell R.M., McGillivray R.T.A.;
"Blood coagulation factor X mRNA encodes a single polypeptide chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence of the light chain of bovine factor X1 (Stuart
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos. NCBI_TaxID=9913;
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MEDLINE=80130563; PubMed=6766735;
Enfield D.L., Bricsson L.H., Pujikawa K., Walsh K.A., Neurath
                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
43-AUG-1987 (Rel. 05, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMullen B.A., Fujikawa K., Kisiel W.; "The occurrence of beta-hydroxyaspartic acid in the vitamin
                                                                                                                                                                                         Score 121; DB 1; Length 456;
Pred. No. 7.1e-13;
9; Mismatches 12; Indels
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CAAF6833F894C209 CRC64;
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Biochem. Biophys. Res. Commun. 115:8-14(1983)
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                                                                                 INTERCHAIN.
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Nucleic Acids Res. 12:4481-4492(1984).
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456
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456 AA;
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                                MEDLINE=94062835; PubMed=8243461;
Inoue K., Morita T.;
"Identification of 0-linked oligosaccharide chains in the activation
peptides of blood coagulation factor X. The role of the carbohydrate
moieties in the activation of factor X.";
Eur. J. Biochem. 218:153-163(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Fitani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
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Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid-containing region.";
J. Biol. Chem. 259:5705-5710(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 41-126.
MEDLINE-96387194; PubMed-8794734;
Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morita T., Jackson C.M.; "Localization of the structural difference between bovine blood coagulation factors X1 and X2 to tyrosine 18 in the activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The relative orientation of Gla and EGF domains in coagulation factor X is altered by Ca2+ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujikawa K., Titani K., Davie E.W.;
"Activation of bovine factor X (Stuart factor): conversion of
"Axa-alpha to factor Xa-beta.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
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Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES
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1122
11655
14992
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86
1125
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P00742; Q14340;
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MOD_RES
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             PUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Subunt: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PACTOR X LIGHT CHAIN.

PACTOR X HEAVY CHAIN.

ACTIVATION PEPTIDE.

ACTIVATED PACTOR XA, HEAVY CHAIN.

MAY BE REMOVED BUT IS NOT NECESSARY FOR ACTIVATION.
                                                                                                                                                                                    PTM: N- AND O-GLYCOSYLATED.

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY).

MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

SIMILARITY: CONCEINE 2 EGF-like domains.
                                                                                                                                        PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlycoSuiteDB; P00743; -.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00742; EGF 2.
InterPro; IPR00509; EGF 11ke.
InterPro; IPR00509; EGF 11ke.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_procease_Try.
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Biochemistry 35:11547-11559(1996)
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                                                                                                                         MORE DISULFIDE BONDS.
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183
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SEQUENCE FROM N.A.
MEDLINE=91216473; PubMed=1902434;
Meseier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
"Cloning and expression in COS-1 cells of a full-length cDNA encoding human coaqulation factor X.";
Gene 99:291-294(1991).
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL) EGF-LIKE 2.
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Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
"Isolation and characterization of human blood-coagulation factor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=85216545; PubMed=2582420;
Fung M.R., Hay C.W., McGillivray R.T.A.;
"Characterization of an almost full-length cDNA coding for human blood coaqulation factor X.";
proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
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MEDLINE=87026600; PubMed=3768336;
Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
"Gene for human factor X: a blood coagulation factor whose gene organization is essentially identical with that of factor IX and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Rieder, Carrington D.P., Chung M.-W., Lee K.L., Czuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 109; DB 1; Length 492;
Pred. No. 8.9e-11;
                                                                                                                                                                                                                                      GAMMA-CARBOXYGLUTAMIC ACID.
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                                                                   SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
GAMMA-CARBOXYGLUTAMIC A
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SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
MEDLINE=94062825; PubMed=8243461;
Inoue K., Morita T.;
"Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moleties in the activation of factor X.";
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Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
"Structural basis for chemical inhibition of human blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                    "Complete amino acid sequence of the light chain of human blood coagulation factor X: evidence for identification of residue 63 as beta-hydroxyagpartic acid.";
Biochemistry 22:2875-2884(1983).
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MEDIJNE=90128299; PubMed=2612918;
Magadeeswaran P., Reddy S.V., Rao K.J., Hamsabhushanam K., Lyman "Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.";
                  McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.
Kwa E.Y., Weinstein B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93360277; PubMed=8355279;
Padmanabhan K.P., Tulinsky A., Park C.H., Bode Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
"Structure of human des(1-45) factor Xa at 2.2-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
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                                                                                                                                                                           MEDLINE=84222026; PubMed=6587384;
Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie J. Characterization of a cDNA coding for human factor X. Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
                                                                                                                                             SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY
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                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 218:153-163(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Mol. Biol. 232:947-966(1993).
[11]
MEDLINE=83257207; PubMed=6871167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 84:517-519(1989).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
-1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTERNSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-1- SIMILARITY: CONTAINS 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular; TAS.
GO; GO:0003804; F:blood coagulation factor X activity; TAS.
GO; GO:0007596; P:blood coagulation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR00143; EGF_2.
InterPro; IPR00143; EGF_II.
InterPro; IPR00143; EGF_II.
InterPro; IPR00203; EGF_II.
InterPro; IPR00203; EGF_II.
InterPro; IPR00203; Vik_dep_GLA.
InterPro; IPR00294; Vik_dep_GLA.
InterPro; IPR00294; Vik_dep_GLA.
IPR001594; Gla; I.
Pfam; PF00009; EGF_IV.
PRINTS; PR00010; EGFBLOOD.
PRINTS; RR00010; EGFBLOOD.
SWART; SM00179; EGF (A; I.
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EMBL; M57285; AAA52421.1; -.
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AAA52636.1;
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MEROPS; S01.216; -.
GlycoSuiteDB; P00742;
Genew; HGNC:3528; F10.
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29-OCT-97.
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M33297;
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1MO6;
1NFU;
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1KYE;
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PDB;
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Genet. 23:373-373(1999).

FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-rhr and then Arg-|-rle bonds in prothrombin to form thrombin.

SUBUNIT: THE TWO CHAINS ARE PORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.
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PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCTUM.
PTM: N- AND O-GLYCOSYLATED.
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20 ANEFLEELRQGTIERECMBEICSYEEVKEVFENKEKTMEFW 60
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019045;
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                                                                 FA10_RABIT
                                                     RESULT 10
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.0%; Score 102; DB 1; Length 231; 41.5%; Pred. No. 5.9e-10;
                                                                                  ch
1 Similarity 43.2%; Pred. No. 1.3e-10;
19; Conservative 8; Mismatches 17: Indela
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                                                                                                                                         1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                         PROTEIN 3. EXTRACELLULAR (POTENTIAL).
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231 CYTOPLASMIC (POTENTIAL).
60 GLA-RICH.
25848 MW; 8A373E4848490D81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF326350; AAK00955.1; -.
HSSP; P00740; 1CFH.
GO; GO:0016021; C:integral to membrane; NAS.
Pfram; PF00594; 91a; 1.
SWART; SM00069; GLA; 1.
PROSTITE; PS00011; GLU_CARBOXYLATION; 1.
PROSTITE; PS0011; GLU_CARBOXYLATION; 1.
PROPEP 1
19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                  PS01187; EGF_CA; 1.
PS00011; GLU_CARBOXYLATION; 1.
PS50240; TRYPSIN_DOM; 1.
 ASX HYDROXYL; 1
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TISSUE=Spinal cord;
                                                                                                    Local Similarity
              PS00022;
PS01186;
 PS00010;
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PROSITE; E
PROSITE; E
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SEQUENCE
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TMG3 HUMAN
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Matches
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                                                                                                                                                                                                                                             MEDLINE=9726311; PubMed=9101642;
Pendurthi U.R., Anderson K.D., James H.L.;
Pendurthi U.R., Anderson K.D., James H.L.;
Pendurthi U.R., Anderson K.D., James H.L.;
Throub. Res. 85:503-514(1997).
-! FUNCTION: Pactor Xa is a vitamin K-dependent glycoprotein that converts prothromain to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-THE bonds in prothrombin to form thrombin.
-!- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM (BY SIMILARITY).
PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
-!- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001818; EGF II.
InterPro; IPR001328; EGF II.
InterPro; IPR002383; GLA blood.
InterPro; IPR002284; Ser protease Try.
InterPro; IPR000294; VitK dep_GLA.
Pfam; PP00098; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM00179; EGF_CA; 1.
SWART; SM00069; GLA; 1.
SWART; SW000020; Tryp SPC; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chymotrypsin.
EGF 2.
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PRINTS; PR00722; CHYMOTRYPSIN.
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STANDARD;
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FA7 RABIT STANDARD; PRT; 444 AA.
P98139; P79224;
01-FEB-1996 (Rel. 33, Created)
15-JUL.1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.

Oryctolagus cuniculus (Rabbit)

conversion accelerator)

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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLECAR, 1.
PROSITE; PS00013; TRYPEIN_HIS; 1.
PROSITE; PS00134; TRYPEIN_HIS; 1.
PROSITE; PS00135; TRYPEIN_HIS; 1.
Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutuanic acid; Hydroxylation; Caid; Hydroxylation; Signal; Zymogen; EGF-like domain; Repeat.
                                                                                                                                  ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
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BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTER N-LINKED (GLCNAC. ...) (POTER N-LINKED (GLCNAC. ...) (POTER N-LINKED (GLCNAC. ...) (POTER N-LINKED)
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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                                                                                                                FACTOR X LIGHT CHAIN. FACTOR X HEAVY CHAIN.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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Best Local Similarity 43.2%;
Matches 19; Conservative
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180
232
232
490
165
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187
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490 AA;
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DOMAIN
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Brothers A.B., Clarke B.J., Sheffield W.P., Blaichman M.A.; "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";

MEDLINE=93190306; PubMed=8383365;

SEQUENCE FROM N.A. NCBI_TaxID=9986;

TISSUE=Liver

Thromb. Res. Suppl. 69:231-238(1993).

REVISION TO 395.

IISSUE=Liver;

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                                                                                                                                                                                                                                                                                                                                                                                                                        form factor Xa.

-!-SUBNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
BY A DISULPIDE BOND (BY SIMILARITY).

-!- TISSUE SPECIFICITY: Plasma.

-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CALCTUM (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-!- SIMILARITY: CONTAINS 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-11e bond in factor X
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InterPro; IPR011881; EGF Ca.
InterPro; IPR001438; EGF II.
InterPro; IPR005209; EGF Ii.e.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002384; GLA_blood.
InterPro; IPR000284; VitK_dep_GLA.
Pfam; PF00594; gla; 1.
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Interpro; IPR001314; Chymotrypsin.
Interpro; IPR000742; EGF_2.
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PRINTS, PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; GEBELOOD.
PRINTS; PR00001; GLABLOOD.
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SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
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Gaps

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Score 101; DB 1; Length 490; Pred. No. 2.1e-09; 8; Mismatches 17; Indels

ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

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RESULT 11

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MEDLINE=91344709; PubMed=2129367; Iwanaga S., Nishimura H., Kawabata S., Kishel W., Hase S., Ikenaka T.; Managa S., Nishimura H., Kawabata S., Kishel W., Hase S., Ikenaka T.; M. and wrisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."; Adv. Exp. Med. Biol. 281:121-1131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U., "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."; Biochemistry 27:7785-7793(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99126518; PubMed=9925787; Zhang E., & Charles R., Tulinsky A.; Extracture of extracellular tissue factor complexed with factor VIIa inhibited with a BPTI mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90062160; PubMed=2511201;
Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
Shimonishi Y., Iwanaga S.,
Identification of a disaccharide (Xyl-Glc) and a trisaccharide
(Xyl2-Glc) O-glycosidically linked to a serine residue in the first
epidermal growth factor-like domain of human factors VII and IX and
protein Z and bovine protein Z.";
J. Biol. Chem. 264:20320-20325(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banner D.W., D'Arcy A., Chene C., Winkler P.K., Guha A.,
Konigsberg W.H., Nemreson Y., Kirchhofer D.;
The crystal structure of the complex of blood coagulation factor
VIIa with soluble tissue factor.";
Nature 380:41-46(1996).
     , Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 MEDLINE=87260948; PubMed=3037537;
O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
Hagen F.S., Murray M.J.;
"Nucleotide sequence of the gene coding for human factor VII, a
vitamin K-dependent protein participating in blood coagulation.",
Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
MEDLINE=11250411; PubMed=1904059;
Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
Komlyama Y., Pedersen A.H., Kisjel W.;
"Human plasma and recombinant factor VII. Characterization of O-
glycosylations at serine residues 52 and 60 and effects of site-
directed mutagenesis of serine 52 to alanine.";
J. Biol. Chem. 266:11051-11057(1991).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445. Rieder M.J., Armel T.Z., Cartington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth B.J., Yi Q., Nickerson D.A.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH MEDLINE-96175641; PubMed-8598903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH
                                                                                                                          Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kisiel W., Kurachi K., Davie E.W.,
                                                                                                                                                                               "Characterization of a cDNA coding for human factor VII.";
Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 61-466, AND POST-TRANSLĄTIONAL MODIFICATIONS.
MEDLINE=89088153; PubMed=3264725;
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                                                                                       TIŠSUB=Liver;
MEDLINE=86205965; PubMed=3486420;
     Eukaryota; Metazoa;
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                       Mammalia; Eutheri
NCBI_TaxID=9606;
     ö
                PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU CARRENTION; 1.
PROSITE; PS00013; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
                                                                                                                                                                                                                                                                                                                            FACTOR IXA, OR THROMBIN) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                BGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FA7 HUMAN STANDARD; PRT; 466 AA.
0104339.
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 42, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
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(GLCNAC. . ) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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HYDROXYLATION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIR
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Pred. No. 2.8e-09;
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SUBSTRATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE.
CLEAVAGE (BY FACTOR XA,
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Best Local Similarity 46.3%;
Matches 19; Conservative
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PS00010;
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014668;
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Marchetti G., Patracchini P., Gemmati D., Derosa V., Pinotti M.,
Rodorigo G., Casonato A., Girolami A., Bernardi F.;
"Detection of two missense mutations and characterization of a repeat
polymorphism in the factor VII gene (F?).";
Hum. Genet. 89:497-502(1992).
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MEDLINE=95072589; PubMed=7981691;
MEDLINE=95072589; PubMed=7981691;
MEDLINE=95072589; PubMed=7981691;
Redeghiero F., Gestaman G., Redaelli R., Pinotti M., Lunghi B.,
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"Topologically equivalent mutations causing dysfunctional coagulation factors VII (294Ala-->Val) and X (334Ser-->Pro).";
Hum. Mol. Genet. 3:1175-1177(1994).
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MEDLINE=9130006; PubMed=2070047;
O'Barien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
Meade T.W., Tuddenham B.G.D.;
"Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected
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Arbini A.A., Mannucci P.M., Bauer K.A.;
"A Thr359Met mutation in factor VII of a patient with a hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caused
                                                                                        "Solution structure of the N-terminal EGF-like domain from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE 94061028; PubMed=8242057;
Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
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"Detection of miseense mutations by single-strand conformational
polymorphism (SSCP) analysis in five dysfunctional variants of
coagulation factor VII.";
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MEDLINE-99367502, Pubmed-9692950;
Mutanyi A., Finn B.E., Gippert G.P., Foreen S., Stenflo J.,
Drakenberg T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95064662; PubMed-7974346;
Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Factor VII Mie: homozygous asymptomatic type I deficiency
an amino acid substitution of His (CAC) for Arg(247) (CGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS CHARLOTTE GLN-139 AND GLN-212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Genet. 2:1355-1359(1993)
                                                                                                      factor VII.";
Biochemistry 37:10605-10615(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thromb. Haemost. 71:773-777 (1994)
Mol. Biol. 285:2089-2104(1999)
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                                                                                                                                                                                                                                                      lood 78:132-140(1991).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Prolinerich Gla protein 1) (Proline-rich Glamma-carboxyglutamic acid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N., Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R., Seligsohn U.; "Alaz44Val is a common, probably ancient mutation causing factor VII deficiency in Moroccan and Iranian Jews."; Thromb. Haemost. 76:283-291(1996).
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MEDLINE-99318093; PubMed=10391209;
Cargill M., Altshuler D., Iraland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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                                                                                                                                                   VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413. MEDILINE-97001216; PubMed-8844208; Bernardi F., Castaman G., Pinotti M., Perraresi P., di Iasio M.G., Lunghi B., Rodeghiero F., Marchetti G.; Mutation pattern in clinically asymptomatic coagulation factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in the signal sequence identified in a patient with factor VII deficiency.";
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HOmo sapines (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98112461; PubMed=9452082;
Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
"Two new missense mutations (P134T and A244V) in the coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Sakuragawa N.;
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deficiency causes defective secretion of the molecule."; Blood 87:5085-5094\,(1996).
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Mutat. Suppl. 1:S189-S191(1998)
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MEDLINE=97037613; PubMed=8883260;
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MEDLINE=97404347; PubMed=9256434;
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Conservative
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        "Primary structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins."; Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).

-I TISSUE SPECIFICITY: Highly expressed in the spinal cord.

-I- PTM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   43.5%; Score 87; DB 1; Length 218; 36.4%; Pred. No. 2.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                             26538A61AB0AEB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                    MIM; 604428; -.. Grantegral to plasma membrane; TAS. GO; GO:005887; C:integral to plasma membrane; TAS. InterPro; IPR002383; GLA blood.
PICHEPRO; IPR000294; VIKT dep_GLA.
PEAM; PF00554; gla; 1.
PRINTS; PR00001; GLABLOOD.
SMART; SM00069; GLA; 1.
PROSTE; PS000011; GLU_CARBOXYLATION; 1.
PROSTE; PRO0011; GLU_CARBOXYLATION; 1.
PROPEP
                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL)
GLA-RICH.
 Davie E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Kulman J.D., Harris J.E., Haldeman B.A.,
                                                                                                                                                                                                                                                                                                                                              PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cDNA sequence of rat prothrombin.";
Nucleic Acids Res. 18:4251-4251(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley, TISSUE-Liver,
MEDLINE-90332426, PubMed-2377469,
Dihanich M., Monard D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92212913; PubMed=1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Banfield D.K., Macgillivray R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                              24947 MW;
                                                                                                                                                                                      EMBL; AF009242; AAB67070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 383-617 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                          Genew; HGNC:9469; PRRG1.
MIM; 604428; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                      83
106
218
61
135
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                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                 HSSP; P00740; 1CFH.
                                                                                                                                                                                                                                                                                                                                                                                                             218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                          carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THRB RAT
                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                   CHAIN
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THRB_RAT
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            OF PROTHROWS TO THROWSIN.

MISCELLANEOUS: PROTHROWS IN SACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & PACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEADVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coaquilation; Plasma; Calcium-binding; Glycoprotein; Repeat;
Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
Hydrolase; Serine protease; Kringle; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE (FRAGMENT ACTIVATION PEPTIDE (FRAGMENT THROMBIN LIGHT CHAIN (A).
characterization of vertebrate prothrombin cDNAs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
SMART; SM00130; KR; 2.
SMART; SM00130; TVP SPC; 1.
PROSITE; PS00011; GLU CARBOXYLATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001383; GLA blood.
InterPro; IPR001383; GLA blood.
InterPro; IPR001364; Prothrombin.
InterPro; IPR001254; Ser protease_Try.
InterPro; IPR001254; VitK_dep_GLA.
Pfam; PF000594; glas; 1.
Pfam; PF000594; kringle; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0722; CHYMOTRYPEIN.
PRINTS; PRO0001; CLABLOOD.
PRINTS; PRO018; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIK; S10511. $10511. HSSP; P00734; 1UVS. MEROPS; S01.217; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
323
359
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Banfield D.K., Macgillivray R.T.;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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. . .) (POTENTIAL).
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MEDLINES=91025551; PubMed=2222810;
Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
"Characterization of the cDNA coding for mouse prothrombin and
localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
                                                                                                                                                                                                                                                                                                                                                                                           42.2%; Score 84.5; DB 1; Length 617; 42.2%; Pred. No. 1.8e-06;
                                                                                                GAMMA-CARBOXYGLUTAMIC ACID.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANS-FLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                       Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
AD27D1B71445DB1D CRC64;
THROMBIN HEAVY CHAIN (B)
                                      CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA)
CLEAVAGE (BY FACTOR XA)
                                                                    CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THRB MOUSE STANDARD; PRT; 618 AA. P19221; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
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SEQUENCE OF 384-618 FROM N.A.
TISSUB=Liver;
MEDLINE=92212913; PubMed=1557383;
                                                                                                                                                                                                                                                                                                                                                                        70411 MW;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.29
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                     617 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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OR CF2
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MOD_RES
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The different species. The species of the B chain of thrombin from amplification and sequence analysis of the B chain of thrombin from nine different species. The species. The different species. The different species. The species of the B chain of thrombin from nine different species. The species of the species of the species. The species of the spe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL. FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y; Glycoprotein; Repeat;
acid; Acute phase; Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTHROMBIN.
ACTIVATION PEPTIDE (FRAGMENT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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PROSITE; PS00011; GLU CARBOXXLATION; 1.
PROSITE; PS00021; KINGLE 1; 2.
PROSITE; PS50070; KRINGLE 2; 2.
PROSITE; PS50070; TRYPSIN DOM; 1.
PROSITE; PS0134; TRYPSIN HIS; 1.
PROSITE; PS0134; TRYPSIN HIS; 1.
Blood coagulation; Plasma; Calcium-binding; Glivitanin K; Zymogen; Gamma-carboxyglutamic acid
Hydrolase; Serine protease; Kringle; Signal.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; GLA blood.
InterPro; IPR000383; GLA blood.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser protease Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfan; PP00594; gla; 1.
Pfan; PP00551; Kringle; 2.
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PRINTS; PR00001; GLABLOOD.
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PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52308; CAA36548.1; -.
EMBL; M81394; AAA40435.1; -.
PIR; A35827; A35827.
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MEROPS; S01.217; -.
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Hydrolase; E
SIGNAL
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(BY SIMILARITY)
          ACTIVATION PEPTIDE (FRAGMENT 2)
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Pred. No. 1.8e-06;
5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                   THROMBIN LICHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
KRINGLE 1.
KRINGLE 2.
SERINE PROTEASE.
CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMICHARGE RELA
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B89F719AAFD601E0 CRC64;
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553 N-
70268 MW;
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Best Local Similarity 42.2%;
Matches 19; Conservative
       553
618 AA;
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CARBOHYD
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Osttro canis famil	Q91wh8 mus musculu	Q99pc6 mus musculu	Q8j002 homo sapien	Q8ixb5 homo sapien	063207 rattus norv	Q8jhc9 brachydanio	Q8n2n6 homo sapien	O54740 mus musculu	Q99132 mus musculu	O88947 mus musculu	Q96pq8 homo sapien	Q8jhc8 brachydanio	Q9gmd9 ornithorhyn	Q@jj40 xenopus lae	Q8nek6 homo sapien
SUMMARIES	, qi	Q9TTR0	Q91WN8	93660	08J002	QBIXBS	063207	Q8JHC9	Q8N2N6	054740	Q99L32	088947	Q96PQ8	овлисв	O9GMD9	Q8JJ40	QBNEK6
	Query Match Length DB	456 6	460 11	460 11	55 4	55 4	482 11	443 13	231 4	481 11	481 11	481 11	701 4	474 13	469 6	229 13	268 4
de	Ouery Match I	75.0	69.5	66.5	63.0	63.0	56.5	51.2	51.0	49.5	49.5	49.5	49.0	47.5	46.5	44.0	43.5
	Score	150	139	133	126	126	113	102.5	102	66	66	66	96	95	93	88	87
	Regult No.		8	m	4	5	9	7	80	თ	10	11	12	13	14	15	16

P83370 hoplocephal Q15253 homo sapien Q16519 homo sapien Q9naG0 homo sapien Q61109 mus musculu	Q8t6i3 halocynthia Q28994 sus scrofa Q91001 gallus gall Q8k3u6 rattus norv	Q95nd7 pan troglod Q95nd6 pan troglod Q29094 sus scrofa Q8jhd0 braachydanio	OSSMEN DOS TAUTUS OSSMEN DOS TAUTUS OSSMEN DOS SADIEN P82807 NOTECHIS SC OSSMEN SETUTATIO CA OSSMEN SADIEN	mus mus mus ratt homo mus brac
P83370 Q15253 Q16519 Q9NSD0 Q61109	QBT613 Q28994 Q91001 Q8K3U6	Q95ND7 Q95ND6 Q29094 Q8JHD0	Q95MB8 Q01XD5 P82807 Q9PTW7 Q81XC5	Q9CQ101 Q9CQW3 Q8BGN6 Q9QVH6 Q9TAS3 Q8T182 Q8AYE4
14441	113	13	1346	111144181
376 100 650 650	542 138 607 446	. 4 4 6 4 4 6 1 1 6 1 6 1 6 1 6 1 6 1 6 1	4 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	226 226 226 1739 1938 673
41.5 41.0 40.0 39.5		37.5	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
88 882 780 79	77.5	75 73 72.5	22772	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
17 18 19 20 21	22 23 2 25 4 36 25	25 25 30 30 30 30	1 W W W W W	2 E E 4 4 4 4 4 4 4 6 8 6 9 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

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NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
099PC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                8 % B B
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                                                                                                       SWART; SW00169; GLA; 1.

R SMART; SW00069; GLA; 1.

R PROSITE; PS00010; ASY HYDROXL; 1.

R PROSITE; PS00109; EGF 1; 1.

R PROSITE; PS001187; EGF 2; 2.

R PROSITE; PS001187; EGF 2; 1.

R PROSITE; PS00119; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN ESR; 1.

W EGF 11ke domain; Hydrolase; Protease; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PROTEIN C LICHT CHAIN.
PROTEIN C CONNECTING DIPEPTIDE.
PROTEIN C HEAVY CHAIN.
7AD3ABC1C34E59FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%; Score 150; DB 6; Length 456; 63.6%; Pred. No. 8.8e-17; ive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 ANSFLEEIRAGSLERECMEEICDFEEAKEIFQNVDDTLAYWSKY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BC013896; AAH13896.1; --- HSSP; P00761; 1AN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPC, 1.
SMORT; SM00020; Tryp_SPC, 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA, 1.
PROSITE; PS01187; GLG_CA, 1.
PROSITE; PS00011; GLG_CARROXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:97771; Proc.
InterPro: IPR00152; Asx hydroxyl.
InterPro: IPR001814; Chymotrypsin.
InterPro: IPR001881; EGF Ca.
InterPro: IPR002209; EGF like.
InterPro: IPR002293; GLA_blood.
InterPro: IPR001294; Ser_protease_Try.
InterPro: IPR001294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 194 PP
195 456 PP
456 AA; 50813 MW;
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TERMBLRel. 19, C)
01-DEC-2001 (TERMBLRel. 19, Le
01-MAR-2003 (TERMBLRel. 23, Le
Similar to protein C.
PROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00089; Erypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.6%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q91WN8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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Q91WNB
ID D1-D1-D
DT O11-D
DT 
    ARABARA RABARA R
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                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                                   Length 460;
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                                                                                                                                                                                           Query Match 69.5%; Score 139; DB 11; Length 4
Best Local Similarity 59.1%; Pred. No. 6.5e-15;
Matches 26; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                              42 ANSFLEEMRPGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 ANSFLEEMRPGSLERECMEEICDLEEAQEIFONVEDTLAFWIKY 85
                                                                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ERR; 1.
ESGF-Like domain; Hydrolase; Protease; Serine protease.
SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Hydrolase; Protease; Serine protease.
SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR001381; EGF Ca.
InterPro; IPR00209; EGF Like.
InterPro; IPR00209; EGF Like.
InterPro; IPR00209; Asr_Drotaase_Try.
InterPro; IPR00209; VitK_dep_GLA.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; Trypsin; 1.
PRINTS; PR00001; GLABLOOD.
SMART; SM00109; EGF_CA; 1.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00100; ASX_HYDROXYL; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF318182; AAK07918.1; -. HSSP; P04070; 1AUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anticoagulant protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:97771; Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=C57BL;
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STRAIN=Sprague-Dawley;
MEDLINE=96091366; PubMed=8578519;
Stanton C., Ross R.P., Hutson S., Wallin R.;
Stanton C., Ross R.P., Hutson S., Wallin R.;
Exidence for competition between vitamin K-dependent clotting factors for intracellular processing by the vitamin K-dependent gamma-
                                                      kattus norvegitus (kat).
Ebkaryota; Metazaa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 113; DB 11; Length 482;
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%; Score 11., 43.2%; Pred. No. 1.7e-10; rive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTIEFWNKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO1187; EGF_CA; 1.
PROSITE; PSO1187; EGF_CA; 1.
PROSITE; PSO1011; GLU_CARBOXYLATION; 1.
PROSITE; PSO10134; TRYPSIN DOW; 1.
PROSITE; PSO01134; TRYPSIN INS; 1.
EGF-like domain; Hydrolase; Protease; Serine protease.
SEQUENCE 482 AA; 54265 MW; 02084678E3954A698 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 Thromb. Res. 80:63-73(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL. 779807; CAA56202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coagulation factor VIIi.
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanumanthaiah R., Day K., Jagadeeswaran P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001881; BGF_G.
InterPro; IPR001881; BGF_G.
InterPro; IPR001438; BGF_II.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
Ifam; PF00008; BGF; 2.
Pfam; PF00089; trypein; 1.
Pfam; PF00189; trypein; 1.
PRINTS; PR00101; GLABLOOD.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chymotrypsin.
EGF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.29
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.216;
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M., Wada Y.,
Kinoshita S., Iida H., Imaaski N.;
"Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
Patients. Genetic Background of Thrombophilia in Japan.";
Submitted (APR-2002) to He EMBL/GenBank/DDBJ databases.
EMBL; AB083700; BAC21172.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Hamasaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,

Kurihara M., Wada Y., Ono M.;

Korihara m., Wada Y., Ono M.;

Gene analysis of anticoagulation factors in Japanese thrombotic

patients.Genetic background of thrombophilia in Japan.";

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO86851; BAC53631.1;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                         Bukaryota, Metazca, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 55;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDT 37
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Pred. No. 1e-13;
                        55 AA
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                        PRT;
                                                                01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Protein C (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                        Homo sapiens (Human)
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SEQUENCE
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Q63207 Q63207;

RESULT 6 Q63207 ID Q632 AC Q632 DT 01-N DT 01-N

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Length 231; 16; Indels

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                                                                                                                                                                                                             1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                   Query Match 51.0%; Score 102; DB 4; Best Local Similarity 41.5%; Pred. No. 5.7e-09; Matches 17; Conservative 8; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
MEDLINE=98454993; PubMed=9783672;
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PS00134; TRYPSIN HIS;
PS00135; TRYPSIN SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Mus musculus (Mouse).
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"Comprehensive analysis of blood coagulation pathways in Teleostei:
Evolution of coagulation factor genes and identification of zebrafish
factor VIIi.";
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InterPro; IPR002383; GLA blood.

InterPro; IPR0054; yitk dep_GLA.

PRINTS; PR00501; GLABLOOD.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FL390093.
Hymo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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SEQUENCE 231 AA; 25844 MW; 8A373BOD5C1D0D81 CRC64;
                                                                                                                                                       231 AA
                                                                                                                                                                                                                                                                                                                                   InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001914; Chymotrypsin.
InterPro; IPR001981; EGF 2.
InterPro; IRR006209; EGF 14ke.
InterPro; IRR0062109; IGF 14ke.
InterPro; IRR0062109; IGF.
InterPro; IRR001254; Ser protease Try.
InterPro; IRR001254; VitK_dep_GLA.
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PROSITE; PS00011; GLU_CARBOXYLATION; 1.
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"Cloning and recombinant expression of mouse coagulation factor X.";
Thromb. Res. 92:33-41(1998).
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                                                                                                                                                                                               Plasmid pBluescript.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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49.5%; Score 99; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 4e-08;
Matches 17; Conservative 9; Mismatches 18; Indels
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41 481 COAGULATION FACTOR X.
481 AA; 53986 MW; CF702DE5EF9D97AE CRC64;
                                                                           01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) cognilation factor X precursor (EC 3.4.21.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thromb. Res. 92:33-41(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AJ222677; CAA10933.1; -.
HSSP; P00742; IXKA.
481 AA
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PS01186; EGF_2; 2.
PS01187; EGF_CA; 1.
PS00011; GLU_CARBOXYLATION; 1.
               054740,
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ant
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InterPro; IPR001481; EGF 2.
InterPro; IPR001481; EGF 7.
InterPro; IPR001481; EGF 11.
InterPro; IPR001293; EGF 11.
InterPro; IPR001294; EGF 12.
InterPro; IPR001254; Ser Drotease Tr InterPro; IPR001254; Ser Drotease Tr EnterPro; IPR001254; Ser Drotease Tr EnterPro; IPR00189; EGF; 2.
Pfam; PP00018; EGF; 2.
Pfam; PP00018; EGF; 2.
Pfam; PR00120; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0001; GLALLING, SMART; SM00179; EGF_CA; I. SMART; SM00069; GLA; I. SMART; SM00020; TYP SPC; I. PROSITE; PS00010; ASX HYDROXY; I. PROSITE; PS00022; EGF_I; I. DPOSITE; PS00022; EGF_I; I.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01186; EGF_2; 2.
PS01187; EGF_CA; 1.
PS00011; GLU CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF 7.
InterPro; IPR001488; EGF 11.
InterPro; IPR001488; EGF 11.
InterPro; IPR001298; EGF 11.
InterPro; IPR001294; EGF 12.
InterPro; IPR001254; Ser protease Tr Pam PP00008; EGF; 2.
Pfam; PP00089; EGF; 2.
Pfam; PP00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR000152; Asx hydroxyl InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00010; ASX HYDROXYL; PROSITE; PS00022; EGF 1: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
SMART; SM0179; EGF_CA; 1.
SMART; SM00069; GIA; 1.
SMART; SM00020; TYPP_SPC; 1.
                                                                                                                                                 Thromb. Haemost. 80:87-91(1998).
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PS00134; TRYPSIN HIS;
PS00135; TRYPSIN SER;
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Best Local Similarity 38.6°
Matches 17; Conservative
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                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                          STRAIN=129SJ
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Q96PQ8
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                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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49.5%; Score 99; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 4e-08;
Matches 17; Conservative 9; Mismatches 18; Indels
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PRINTS; PR00123; CHYMOTRYPESIN.
PRINTS; PR001010; EGFBLOOD.
PRINTS; PR001010; EGFBLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS001010; ASX HYDROXYL; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS011186; EGF_2; 2.
PROSITE; PS011181; EGF_CA; 1.
PROSITE; PS01011; GLUCARBOXYLATION; 1.
PROSITE; PS01013; TRYPSIN DOM; 1.
PROSITE; PS01013; TRYPSIN DOM; 1.
PROSITE; PS01013; TRYPSIN HIS; 1.
PROSITE; PS01013; TRYPSIN HIS; 1.
PROSITE; PS01013; TRYPSIN SER; 1.
41 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
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                                                                                                                                                                                                                                             Strausberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL. BCO03477; AAH03877.1; -.
HSSP; PO0742; 1XKA.
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                          Last sequence update)
Last annotation update)
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; CGF 2.
InterPro; IPR001881; EGF 7.
InterPro; IPR001438; EGF II.
InterPro; IPR0012383; GGF II.
InterPro; IPR0012383; GLA blood.
InterPro; IPR0012383; GLA blood.
InterPro; IPR001234; VitK dep_GLA.
Pfam; PP000084; BGF; 2.
                                                                                              Created)
                                                                   PRT;
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                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                            MEROPS; S01.216; -.
MGD; MGI:103107; F10.
                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                     Coagulation factor X
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=10090;
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01-NOV-1998 (
01-MAR-2003 (
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                                   RESULT 11
088947
1D 08894
DT 01-NO
DT 01-NO
DT 01-MA
DE COSQU
GN F10.
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Gaps
SEQUENCE FROM N.A.
STRAIN=CSTBLE X CBA, TISSUB=Liver,
STRAIN=CSTBLE X CBA, TISSUB=Liver,
MEDLINE-99347931, bubMed=9684791,
Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
Castellino F.J., Rosen E.D.,
"Cloning and characterization of a cDNA encoding murine coagulation factor X.",
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SIGNAL 1 40 POTEWTIAL.
CARGULATION 41 481 CARGULATION X.
SEQUENCE 481 AA, 54018 MW, 8ACO9DESEF9D271E CRC64,
                                                                                                                                                                                                                                                                                                                                                         Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
"Cloning and Characterization of the Murine Factor X Gene.";
Thromb. Haemost. 0:0-0(2000).
INILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AF087644; AAC36545.1;
EMBL; AF087644; AAC36545.1;
HSSP; D00422; IXKA.
MSROPS; S01.216;
MGD; MGI:103107; FIO.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Factor VII active site mutant immunoconjugate.
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Hanumanthaiah R., Day K., Jagadeeswaran P.;
"Comprehensive analysis of blood coagulation pathways in Teleostei:
Evolution of coagulation factor genes and identification of zebrafish
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MEDLINE=21015017; PubMed=11132153;
Poorafshar M., Aveskogh M., Munday B., Hellman L.;
Ildentification and structural analysis of four serine proteases in immonotreme, the platypus, Ornithorhynchus anatinus.";
Immunogenetics 52:19-28(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ornithorhynchus anatinus (Duckbill platypus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 474;
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SEQUENCE 474 AA; 53580 MW; E1E18C1E54F27532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 95; DB 13;
40.9%; Pred. No. 1.9e-07;
tive 7; Mismatches 19
                                                                            -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL, AP275654; AAG00453.1, -.
HSSP; P00742; 1XXB.
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                                                                                                                                                                                                                                    InterPro; IPR00142; GGF_Z.
InterPro; IPR00143; GGF_Z.
InterPro; IPR001438; EGF_T.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; GIA_blood.
InterPro; IPR0062383; GIA_blood.
InterPro; IPR001254; SGF_E.
InterPro; IPR001254; SGF_Drotease_Try.
InterPro; IPR001254; SGF_Drotease_Try.
Pfam, PF00089; GGF; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR0010; EGFBLOOD.
PRINTS; PR00101; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00011; GLU CARBOXYLATION; 1
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SMART; SW00179; EGF CA; 1.
SMART; SW00069; GLA; 1.
SMART; SW00020; Tryp SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
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InterPro; IPR001314; Chymctrypsin.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50240; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN SER; 1.
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les 18; Conservative
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Matches
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Q9GMD9
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                                                                                                                                                                                   Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 9e-08;
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PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Hydrolaes; Protease; Serine protease.
SEQUENCE 701 AA; 77826 MW; 94ACGCEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 AA
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Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF_2; 1.
EGF_CA; 1.
GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003597; Ig_cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001254; Ser_procease_Try.
Interpro; IPR000294; Vitk_dep_GLA.
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SMART; SMO0179; BGP_CA; 1.
SWART; SM00069; GLA; 1.
SWART; SM00407; IGc1; 1.
-SWART; SM00300; TYP, SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                          SEQUENCE FROM N.A. MEDLINE=21477448; Pubmed=11593034;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO01881; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR0052383; GLA_blood.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00089; trypain, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.8%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gla;
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NCBI_TaxID=7955;
                                                                                                                                                                Hu Z., Garen A.;
                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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[1] SEQUENCE FROM N.A

RESULT 13
08JHC8
1D 08JHC
AC 08JHC
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DT 01-MC
DT 01-MC
DT 0C OS
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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"A STATE OF THE CARROLL OF THE CARRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%; Score 93; DB 6; Length 469; ilarity 40.5%; Pred. No. 4.1e-07; Conservative 6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Last annotation update)
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Georgi A.B., Stukenberg P.T., Kirschner M.W.;
"Timing of events in mitosis.";
Curr. Biol. 12:105-114(2002).
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InterPro; IPR002383; GLA blood.
InterPro; IPR00294; Vitk_dep_GLA.
PRam; PPR00594; Gla; 1.
PRINTS; PR00001; GLABLOOD.
SMART; SM00069; GLA: 1.
PROSITE; PS00011; GLU CARBOXYLATION; 1.
PROSITE; PS00011; GLU CARBOXYLATION; 1.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Xenopus laevis (African clawed
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Best Local Similarity 34.19
Matches 15; Conservative
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01-MAR-2003 (TrEMBLrel.
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SEQUENCE
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Run on:

Scoring table:

Searched:

Database :

Result No.

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NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08955636A
| Patent No. 6017882 |
| GENERAL INFORMATION: APPLICATION: APPLICATION: MODIFIED VITAMIN K-DEPENDENT TITLE OF INVENTION: POLYPEPTIDES |
| TITLE REFERENCE: 09531/002001 |
| CURRENT APPLICATION NUMBER: US/08/955,636A |
| CURRENT FILING DATE: 1997-10-23 |
| NUMBER OF SEQ ID NOS: 35 |
| SEQ TWARE: FASESEQ for Windows Version 3.0 |
| LENGTH: 44
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US-08-955-636-24

i Sequence 24, Application US/08955636A

i Betnet No. 6017882

i GENERAL INFORMATION:
    APPLICANT: Nelsestuen, Gary

ITILE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT:
    TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT APPLICATION NUMBER: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

88.0%; Score 176; DB 3;
Best Local Similarity 97.7%; Pred. No. 1.6e-22;
Matches 43; Conservative 0; Mismatches 1;
                                                                                    US-08-955-636-2
US-08-330-978-2
US-08-444-692-2
US-08-774-692-2
US-08-774-592-2
US-08-487-037-2
US-08-487-037-1
US-08-469-486-53
US-08-469-486-53
US-08-469-486-2
US-08-469-486-2
                                                                                                                                                                                                                                                                                                              US-08-469-486-2
US-08-469-658-2
US-08-295-411-3
US-08-955-471-3
                                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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QRGANISM: Homo sapiens
FEATURE:
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Sequence 21, Appl
Sequence 25, Appl
Sequence 1, Appli
Sequence 4, Appli
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Sequence 2, Appli
Patent No. 5270178
Sequence 5, Appli
Sequence 1, Appli
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Sequence 24, Appl
Sequence 35, Appl
Sequence 1, Appli
                                                                                                                                               December 30, 2003, 09:17:31 ; Search time 21 Seconds (without alignments) 88.651 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(c) 1993 - 2003 Compugen Ltd.
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US-08-955-636-35
US-08-955-636-35
US-08-955-636-35
US-08-955-636-10
US-08-955-636-21
US-08-955-636-21
US-08-955-636-21
US-08-955-636-21
US-08-955-411-1
US-08-956-956-2
US-08-756-506-2
US-08-756-506-4
SZ70178-13
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5270178-2
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US-09-065-872-1
                                                                                                                                                                                                                                                                                                                                                                                                     328717 segs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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NAME/KEY: MOD_RES

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7 CTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 168; DB 3; Length 44
Pred. No. 3.5e-21;
0; Mismatches 2; Indels
                      1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ANSFLXXLROSSLXRXCIXXICDFXXARXIFEDVDDTLAFWSKH 44
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                                                                                                                                                   Sequence 20, Application US/08955636A

Sequence 20, Application US/08955636A

Batent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT PELLING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1. Application US/08955636A
Fatent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/00201
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 21
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.5%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (0)...((
                                                                                                                    RESULT 5
US-08-955-636-20
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                                                                                                                                                                  Gaps
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                 LOCATION: (0) ... (0)
CTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LOCATION: (0) ... (0)
1 OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCATION: (0) ... (0) ... (0) ... OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                               Query Match 87.0%; Score 174; DB 3; Length 44; Best Local Similarity 97.7%; Pred. No. 3.5e-22; Matches 43; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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US-08-955-636-1

Sequence 1, Application US/08955636A

Setent No. 6017882

GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/0020D1

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SECTION OF SECTION NOS: 35

SECTION OF SECTION NOS: 35

SECTION OF SECTION NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
PAPLICANT: Nelsestuen, Gary
ITLE OF INVENTION:
PITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-955-636-35
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Gaps

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US-08-955-636-25
Sequence 25, Application US/08955636A
; Patent No. 6017882
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NAME/KEY: Region
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ZIP: 92037
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. OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636;25
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                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 84.0%; Score 168; DB 3; Length 44; Best Local Similarity 95.5%; Pred. No. 3.5e-21; Matches 42; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATE:
APPLICATION NUMBER: US/08/965,832
FLING DATE: 7-NOV-1997
CLASSITCATION DATA:
APPLICATION NUMBER: 08/745,254
FLING DATE: 8-NOV-1997
APPLICATION NUMBER: 60/053,768
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: PADEC, PATERE L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08965832
Patent No. 5847085
GENERAL INFORMATION:
APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV TITLE OF INVENTION: Modified Protein C NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Aliantic Center, 1201 West
APPLICANT: Nolsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FITLE OF INVENTION: POLYEPTIDES
FILE REPERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT PILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 45 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Atlanta
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US-08-965-832-2
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GENERAL INFORMATION:

APPLICANT: Griffin, John H.

APPLICANT: Graffin, John H.

APPLICANT: Mesters, Rolf M.

TITLE OF INVENTION: Serine Protease-Derived Polypeptides and

TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods

TITLE OF INVENTION: for Inhibiting Coagulation

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                   LOCATION:
, OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-965-832-2
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0
                                                                                                                                                                                                                                                                                    Length 45
                                                                                                                                                                                                                                                                              Query Match 84.0%; Score 168; DB 2; Length 45
Best Local Similarity 93.2%; Pred. No. 3.6e-21;
Matches 41; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION : 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: TSRIZ63.0C1
TELEPHONE: 619-554.2937
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OTHER INFORMATION: /note= "Protein C Light Chain"
NAME/KEY:

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note= "where Kaa means gamma OTHER INFORMATION: carboxylglutamic acid"

PEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08295411
Patent No. 5679639
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Region
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Length 419;

Score 168; DB 2; Length 41 Pred. No. 4.4e-20; 2; Mismatches 10; Indels

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/note= "Protein C Heavy Chain"
OTHER INFORMATION: Peptide'
                                                                                                                                          Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
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                                                          LOCATION: 170..419
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
          FEATURE:
NAME/KEY: Region
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                                                84.0%; Score 168; DB 1; Length 419; llarity 72.7%; Pred. No. 4.4e-20; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                         1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC
                                                                                                LOCATION: 170..419
COTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-295-411-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation
                       /note= "Protein C Activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INDORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Proteas
TITLE OF INVENTION: for Inhibiting
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFRENCE/POCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                   Peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 419 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                  OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Region
                                                                             NAME/KEY: Region
                                                                                                                                                                                                     Local Similarity
tes 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 92037
  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-955-471-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                    Query Match
                                                          FEATURE:
                                                                                                                                                                                                     Best Loc
Matches
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APPLICANT: Griffin, John H. APPLICANT: Mesters. Rolf TITLE OF INVENTION: Relie Protease-Derived Polypeptides and TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods TITLE OF INVENTION: for Inhibiting Coagulation WIMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Jeffrey C
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
URRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/045,255
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEC ID NOS: 3
SOFTWARE: Patentin version 3.1
SEC ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                              1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDFLAFWSKH 44
1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 168; DB 4;
Pred. No. 4.4e-20;
2; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9210242 GENERAL INFORMATION:
                                                                                                                                                                                                    Sequence 3, Application US/09667570A Patent No. 6436397 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

Best Local Similarity 72.7%;
Matches 32; Conservative
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Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-756-506-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-756-506-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 32; Conserva
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STREET: Lav.
TTV: Seattle
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Pred. No. 4.4e-20;
2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Protein C Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Protein C Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Protein C Activation
Peptide"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-N0V-1991
ATTONREV, GEBNT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                       TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 84.0%;
1 Similarity 72.7%;
32; Conservative ;
19921118
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                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /
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COTHER INFORMATION:
PCT-US92-10242-1
                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.157
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
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LOCATION: 170..4
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Best Local Similarity
Matches 32; Conserv
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STREET: 12
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                                                                                                                                                                                                                                                                                                      Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                            43 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APFLICANT: Sprecher, Cindy A.
APFLICANT: Prunkard, Donna B.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
                                                                                                                                                                                                                                                                                                      ; DB 2;
4.9e-20;
                                                                                                                                                                                                                                                                                                  Score 168; DB:
Pred. No. 4.9e-:
2; Mismatches
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08756506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZymoGenetics, Inc
ATTORNEY/AGENT INFORMATION:
NAME: Sawielak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-
TELECOMMUNICATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Garner, Ian
: Cottingham, Ian R.
: Temperley, Simon M
: Foster, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 9:
TELECOMMUNICATION INFORMATION
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                  84.0%;
milarity 72.7%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,43
                                                                                                              TELEFAX: 206-542-6678
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 460 amino acide TYPE: amino acide TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 amino acids
amino acid
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Search completed: December 30, 2003, 09:20:38 Job time: 22 secs

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1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

2, Appli 3, Appli 1, Appli 7, Appli 1, Appli 1, Appli 1, Appli 4, Appli 23, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence

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Run on:

Searched:

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Sequence

Sequence Sequence

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Sequence 18,

sequence Sequence

Sequence Sequence

Sequence Sequence

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1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Pred. No. 3.2e-22;
0; Mismatches 9;
US-10-298-330-2
US-10-348-504-44
US-10-348-504-44
US-10-298-330-18
US-10-298-330-3
US-10-375-741-14
US-10-375-741-14
US-10-398-330-3
US-10-288-330-3
US-10-288-330-4
US-10-298-330-2
US-10-298-330-2
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US-10-288-495-43
US-10-188-495-43
US-10-188-495-40
US-10-189-123-42
US-10-189-123-43
US-10-189-123-43
US-10-189-123-43
US-10-189-123-43
US-10-189-123-43
US-10-189-123-43
US-10-189-123-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
TILE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT FILING DATE: 2002-11-04
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10168407
Publication No. US2003020743541
GENERAL INFORMATION
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 79.5%;
Matches 35; Conservative
                                                                                                                                             ORGANISM: Homo sapiens
      LENGTH: 419
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US-10-168-407-4
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      TYPE: PRT
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                                                                                                                                                                    (without alignments)
282.476 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
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| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
                                                                                                                                                                                                                                                                 1 ANSFLXXLRHGSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH
                                                                                                                                             December 30, 2003, 09:19:36 ; Search time 31 Seconds
                         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-168-407-4
US-10-168-407-4
US-10-182-263-3
US-10-182-263-5
US-10-182-263-5
US-10-168-407-5
US-10-168-407-6
US-10-168-407-6
US-10-168-407-6
US-10-182-263-6
US-10-182-263-6
US-10-182-263-1
US-10-182-263-1
US-10-182-263-1
US-10-168-407-1
US-10-168-407-1
                                                                                                                                                                                                                                                                                                                                                                                                        Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                      724715 segs, 199017464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                           US09497591-1EDITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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Match Length DB
                                            Copyright
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91.0
87.0
87.0
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: 24, Appl 8, Appli 2, Appli 116, App

Sequence Sequence 3

Sequence Sequence Sequence

Sequence Sequence ö

Gaps

. 0

44

Length 419; Indels

Result

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Gaps

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Length 419;

Score 182; DB 15; Pred. No. 3.2e-22; 0; Mismatches 9;

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91.0%;
                                            Query Match
Best Local Similarity 79.59
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5
LENGTH: 419
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    US-10-182-263-4
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APPLICANT: Gerlitz, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Gerinnell, Brian W
FILE REFERENCE: X-13611
CURRENT APPLICATION UNDRER: US/10/182, 263
CURRENT APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-07-22
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PAECHIN version 3.1
SEQ ID NO 4
LENGTH: 419
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3. Application US/10182263
Publication No. US2030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-1541
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR PLICATION NUMBER: 60/181948
PRIOR PLLING DATE: 2000-03-11
PRIOR PPLICATION NUMBER: 60/18199
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CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin vergion 3.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT
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SCATWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                             ORGANISM: Homo saplens
US-10-168-407-4
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 35; Conserv
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1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                       1 ANSFLEBLRHGSLERECIEBICDFBEAKBIFEDVDDTLAFWSKH 44
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Pred. No. 3.2e-22;
0; Mismatches 9;
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CURRENT FILING DATE: 2002-11-04

CURRENT FILING DATE: 2002-11-04

CURRENT FILING DATE: 2002-11-04

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

SEG ID NO SEG ID NOS: 12

LENGTH: 419
                                                                                                                                                                                                                 APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bryan E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/18199
PRIOR PILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/18199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                                                                                                                               US-10-182-263-5
; Sequence 5. Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
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Best Local Similarity 79.5%;
Matches 35; Conservative
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Best Local Similarity 77.3%;
Matches 34; Conservative
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RESULT 7

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84.0%;
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 1, Application US/10298330

Sequence 1, Application US/10298330

Publication No. US20030100506A1

GENERAL INFORMATION:

TITLE OF INVENTION: Modified Vitamin K-Dependent

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 09531-127001

CURRENT APPLICATION NUMBER: US/10/298,330

CURRENT FILING DATE: 2002-11-18

PRIOR PILING DATE: 2000-02-03
Sequence 6, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OP INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER: OF SEQ ID NOS: 12
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10182263
| Publication No. US20030022354A1
| GENERAL INFORMATION:
| APPLICANT: Gerlitz, Bruce E
| APPLICANT: Grinnell, Brian W
| TILE REPERENCE: X-13611
| CURRENT FILING DATE: 2002-07-22
| CURRENT FILING DATE: 2002-07-22
| PRIOR APPLICATION NUMBER: 60/181948
| PRIOR PILING DATE: 2002-02-11
| PRIOR PILING DATE: 2002-03-14
| NUMBER: OF SEQ ID NOS: 12
| SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                          LENGTH: 419
TYPE: PRT
CRGANISM: Homo sapiens
US-10-168-407-6
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LENGTH: 419
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US-10-182-263-6
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| Sequence 4, Application US/09978917A
| Publication No. US20030027299A1
| GENERAL INFORMATION:
| APPLICAMT: Maxygen Holdings
| TITLE OP INVENTION: Protein C or activated protein C-like molecules
| FILE REPERENCE: 0219us310 - protein C
| CURRENT APPLICATION NUMBER: US/08/978, 917A
| CURRENT FILING DATE: 2001-10-17
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 4
| SEQ IP NO
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NAME/KEY: VARIANT

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29

CTHER INFORMATION: Xaa = gamma carboxyglutamic or glutamic acid
US-10-298-330-1
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84.0%; Score 168; DB 11; Length 419;
Best Local Similarity 72.7%; Pred. No. 7.3e-20;
Matches 32; Conservative 2; Mismatches 10; Indels
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Pred. No. 7.3e-20;
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84.0%; Score 168; DB 15;
Best Local Similarity 93.2%; Pred. No. 6.1e-21;
Matches 41; Conservative 2; Mismatches 1;
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Publication No. US20030207435A1

GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 419
PRIOR APPLICATION NUMBER: 09/302,239
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 44
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43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 86
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Pred. No. 8.1e-20;
2; Mismatches 10;
                               Sequence 2, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPREBNCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION: APPLICANT: Gerlitz, Bruce E
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-182-263-2
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10; Indels
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                                      1. ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Pred. No. 8.1e-20;
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Pred. No. 7.3e-20;
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Mismatches
                                                                                                                                                                                                                                                             APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPERRICE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maxygen Aps, Maxygen Holdings
TITLE OF INVENTION: Protein C or activated
FILE REFERENCE: 021948310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09978917A, Publication No. US20030027299A1, GENERAL INFORMATION:
                                                                                                                                                                                Sequence 1, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
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72.7%;
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Best Local Similarity 72.73
Matches 32; Conservative
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32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-10-182-263-1
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; LOCATION: (43)...(461)
US-09-978-917A-2
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Best Local Similarity
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US-09-978-917A-2
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Pred. No. 8.1e-20;
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APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR PELING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
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Job time : 32 secs
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